



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96364

TO: Daniel Sullivan
Location: CM1/12D12/11E12
Art Unit: 1636
Wednesday, June 25, 2003

Case Serial Number: 982091

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Sullivan,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library, CM1-1E01 Desk



CDS

precursor cells treated 2-weeks mitotic inhibitor after
5-weeks retinoic acid (RA) induction.-majorly NR2 neuron*
489..1178

/note="unnamed protein product"

/codon_start=1

/protein_id="BAC04755.1"

/db_xref="GI:21755765"

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RAAPSRPODA"

BASE COUNT 658 a 716 c 907 g 653 t

ORIGIN

Query Match 1.7%: Score 484; DB 9; Length 2914;

Best local similarity 100.0%; Pred. No. 1.3e-239;

Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 25614 AGCAGCGACAGAGCCCCCGGCTACCGCCTTAGGGGTTTCCCGGGGGTGGGAAGCCAT 25673
DB 1 AGCAGCGACAGAGCCCCCGGCTACCGCCTTAGGGGTTTCCCGGGGGTGGGAAGCCAT 60
OY 25674 TGAGAGATTAAACCCCGGAGGTGCTGACTAATCAAGATTTCCTTGAATAATGCAAGGTG 25733
DB 61 TGAGAGATTAAACCCCGGAGGTGCTGACTAATCAAGATTTCCTTGAATAATGCAAGGTG 120
OY 25734 TCTCGAGGAGGCTAATGATGAGGAAGGCCAGGAATGCCAATAGAGAGACAGCGG 25793
DB 121 TCTCGAGGAGGCTAATGATGAGGAAGGCCAGGAATGCCAATAGAGAGACAGCGG 180
OY 25794 ACCTGGAAGGCTGGGCTCAACCGGCGCCCGCGGGGCGCAAGCCGTTCCCGCCAGAGGG 25853
DB 181 ACCTGGAAGGCTGGGCTCAACCGGCGCCCGCGGGGCGCAAGCCGTTCCCGCCAGAGGG 240
OY 25854 CTTGCGCGGGGCTCGCGGGGAAACCGAACCGCCACAGTGGAGACCGTCCGCTCCGCCCT 25913
DB 241 CTTGCGCGGGGCTCGCGGGGAAACCGAACCGCCACAGTGGAGACCGTCCGCTCCGCCCT 300
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DB 301 GCTGCGGACAGCCCGCTGACTCGCAGTCCGGGACTGGGCGCTGGCCGCTCCCGGGA 360
OY 25974 GCCCGGACCGAGCGCTGAGCGCGGAGAACCGCCAGCGGCGGAGAACCCCGACCGAGGGA 26033
DB 361 GCCCGGACCGAGCGCTGAGCGCGGAGAACCGCCAGCGGCGGAGAACCCCGACCGAGGGA 420
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DB 421 CTAGACACACACAGCGCGCGGCGAGACAGACCGACCGCCGAGGCGGCGCTCTAC 480
OY 26094 GCCG 26097
DB 481 GCCG 484

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RESULT 5

BC026909

LOCUS BC026909 2579 bp mRNA linear PRI 08-APR-2002

DEFINITION Homo sapiens, hypothetical gene LOC127703, clone MGC:24981

ACCESSION IMAGE:4932944, mRNA, complete cds.

VERSION BC026909.1 GI:20071213

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2579)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (04-APR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK

COMMENT

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgaphs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amgdbcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,

Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Munzy, D.M.,

Richards, S., Glibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 29 Row: n Column: 8

This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analyses.

FEATURES

SOURCE

location/Qualifiers

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/clone="MGC:24981 IMAGE:4932944"
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CDS

BASE COUNT

605 a 598 c 771 g 605 t

ORIGIN

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Best local similarity 100.0%; Pred. No. 1.1e-175;

Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 28477 GCTGATGTTCCGATCCAGGCTACGAGGCTGAGGGGGCCAAATTCCTGGGAGCCAC 28536
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DB 175 CTCCTGATTATGTCACGCCGAGCTCCACAGCAGACCACTCACTTATGGAAGTG 234
OY 28597 CCAAGATGCTTAACGAGAAATTTGGATGGATGGCCAGCAGAGTGAAGCTATCTGAGGA 28656
DB 235 CCAAGATGCTTAACGAGAAATTTGGATGGATGGCCAGCAGAGTGAAGCTATCTGAGGA 294
OY 28657 GGAAGCTCTCTGATGATACCTCTGACAAACCAACCTTCCAGGCGCTGATCCCTGAGG 28716
DB 295 GGAAGCTCTCTGATGATACCTCTGACAAACCAACCTTCCAGGCGCTGATCCCTGAGG 354
OY 28717 AAGGGTGGCCAGCCCGCCAGAGGGGCGACAGATTCCCGGCGCTGAGCCTGAGAACATGG 28776
DB 355 AAGGGTGGCCAGCCCGCCAGAGGGGCGACAGATTCCCGGCGCTGAGCCTGAGAACATGG 414
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Matches 1286; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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62528 ATATGATCCAGCAATTTTCACTTCTAGTCTGTACCCCAAAAGAGTGAAGCAGGACTTGA 62587
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Db |||||||
62588 ACAGATATTTGCAACCCCATGTTCAAGCAGCATTATTCACAGTAAGTAGTCAAAACATG 62647
QY 121 AAAGCGACCTATGTTTATTTGGCAATGAATGGTAAACAAATGCGGTATATATGCAAG 180
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62648 AAAGCGACCTATGTTTATTTGGCAATGAATGGTAAACAAATGCGGTATATATGCAAG 62707
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62768 ACACCTTTGGTGGCTGAGTGGCGCATCACTTGAGCTCAGAGTTTGAGCCAGCCTGG 62827
QY 301 ATAATATGCAAAACCCATCCCTATAAAAAATACTAAAAATAGCTAGGCGTGGCG 360
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62888 GCAGTACCAAGCTATTACAGGGGCTGAGTGGGAGAAATTCCTTGAGCCTGGGAGGCAATG 62947
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63008 AAAAAAAGAGTTCTGACACTTTGCTACACATGGATGAACCTTTAGAAATGTTATGCTAAAA 63067
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QY 781 GCAATTTTATATGCTATTTTACCACAAATGCAAAATTTAAAAATTTTCTCCGT 840
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63307 GCAATTTTATATGCTATTTTACCACAAATGCAAAATTTAAAAATTTTCTCCGT 63366
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RESULT 4
AK096303
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DEFINITION AK096303
ACCESSION AK096303.1 GI:21755764
VERSION oLlgo capping; fis (full insert sequence);
KEYWORDS Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
SOURCE clone_lib:NT2R12 clone:NT2R12005579.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodeira,H., Furiya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kanihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEO human cDNA sequencing project
Unpublished
2 (bases 1 to 2934)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI); cDNA library
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
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Oy 6579 AAGGAAACAAATACCCAGAGACCTGATTCACAAATCCAGGAGGATGATTAATAG 6638
Dh 66929 AAGGAAACAAATACCCAGAGACCTGATTCACAAATCCAGGAGGATGATTAATAG 66870

* 101710 101809: gap of 100 bp
 * 101810 107002: contig of 5193 bp in length
 * 107003 107102: gap of 100 bp
 * 107103 111862: contig of 4760 bp in length.

FEATURES

source

Location/Qualifiers
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 1. 6110

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misc_feature

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misc_feature

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misc_feature

/note="assembly_fragment:00880"
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BASE COUNT 31378 a 23312 c 23424 g 32240 t 1508 others
 ORIGIN

Query Match 16.0%; Score 4624; DB 2; Length 111862;
 Best Local Similarity 99.7%; Prod. No. 0;
 Matches 5934; Conservative 0; Mismatches 7; Indels 9; Gaps 7;

QY 3159 ATTTATTTTAGGATATTTAAAGAAATACAAACTGGGTGCGAGTGGCCCGCCCTATATCT 3218
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DB 70168 AGTGCCTGTAAATCCAGCTACTCAGGAGGCAAGCTGGAGATCGCTTGAACCGGAGGT 70109
 QY 3399 GGAGGTCAGTGAGCTGAGATTGCGATTGCGATTCAGCCTGGCGCAGAGAGAACT 3458
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 DB 69928 ATATTTTATATAGTTGAGATTGTAACAATCTTTCTATATGATAAATTTTGCATCTTTT 69869
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DB 97528 GCGTGGACTGTTATGTAAGATTTGAGAGACATATGTTGGTTCAGGGTTGATAGCAG 27587
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OY 28321 AACCAAGAGGAACTGTTACACAGTCAAGAGAAAGGCTTGACAGGAGTGGCCAGC 28380
DB 97768 AACCAAGAGGAACTGTTACACAGTCAAGAGAAAGGCTTGACAGGAGTGGCCAGC 27827
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DB 98128 ACAACCAAGCCTTCAGAGCCCTGATGATCCCTGAGAGAGAGGTCGAGCCCGCAGAG 28187
OY 28741 GGGCAGAGATTCGGGGGCTGAGCCTGAGAAAGATGGTGTGTCGACAGCTCTGCTCC 28800
DB 98188 GGGCAGAGATTCGGGGGCTGAGCCTGAGAAAGATGGTGTGTCGACAGCTCTGCTCC 28247
OY 28801 CTCTGAGAGACAGGCTATGCTACAGCACTTCCCTGAG 28837
DB 98248 CTCTGAGAGACAGGCTATGCTACAGCACTTCCCTGAG 98284

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RESULT 2
AL139143/c
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DEFINITION
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SEQUENCING IN PROGRESS ***; 16 unordered pieces.
ACCESSION
AL139143
VERSION
AL139143.6 GI:9863524
KEYWORDS
HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 111862)
Plumb, B.
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerequests@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9212183.
-----
Center: Sanger Centre
Genome Center
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
Project Information
Center project name: dJ555P23
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Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 105109 bases at least Q40
Consensus quality: 107835 bases at least Q20
Consensus quality: 109154 bases at least Q20
Insert size: 110362; sum-of-contrigs
Insert size: 138096; 6.8% error; agarose-fp
Quality coverage: 3.57x in Q20 bases; sum-of-contrigs quality
coverage: 3.11x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 6110: contrig of 6110 bp in length
* 6111 6210: gap of 100 bp
* 6211 12365: contrig of 6155 bp in length
* 12366 12465: gap of 100 bp
* 12466 14908: contrig of 2443 bp in length
* 14909 15008: gap of 100 bp
* 15009 17724: contrig of 2716 bp in length
* 17725 17824: gap of 100 bp
* 17825 25035: contrig of 7211 bp in length
* 25036 25135: gap of 100 bp
* 25136 27936: contrig of 2801 bp in length
* 27937 28036: gap of 100 bp
* 28037 31938: contrig of 3902 bp in length
* 31939 32038: gap of 100 bp
* 32039 44844: contrig of 12806 bp in length
* 44845 44944: gap of 100 bp
* 44945 57247: contrig of 12303 bp in length
* 57248 57347: gap of 100 bp
* 57348 63813: contrig of 6466 bp in length
* 63814 63913: gap of 100 bp
* 63914 70362: contrig of 6449 bp in length
* 70363 70462: gap of 100 bp
* 70463 80246: contrig of 9784 bp in length
* 80247 80346: gap of 100 bp
* 80347 94000: contrig of 13654 bp in length
* 94001 94100: gap of 100 bp
* 94101 101709: contrig of 7609 bp in length

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Db	96448	CTGACTCTGGGGAATATGATGGAGGATATATACAGAGGTCCCAAGCCAGATTTACAAC	96507	
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Qy	27181	GGGACCCAGAGAGGCAATACTTAACCGTCTGTTTATTAATATGATTTGAGTGGGCACT	27240	
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24348 CACTTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 94407
24961 GGACATGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 25020
|||||
24408 GGACATGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 94467
25021 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 25080
|||||
24468 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 94527
25081 GTGGGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 25140
|||||
24528 GTGGGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 94587
25141 CAGGCTCCCAAGTGTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 25200
|||||
24588 CAGGCTCCCAAGTGTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 94647
25201 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 25260
|||||
24648 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 94707
25261 GTTATCTGCGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 25320
|||||
24708 GTTATCTGCGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 94767
25321 GGCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25380
|||||
24768 GGCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 94827
25381 AATGCTATGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 25440
|||||
24828 AATGCTATGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 94887
25441 AGTCAGAGATCTCTCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25500
|||||
24888 AGTCAGAGATCTCTCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 94947
25501 TGTCTAGACCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25560
|||||
24948 TGTCTAGACCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 95007
25561 GTTAACTGCGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25620
|||||

D	b	90628	AAGTAAGCACCTCTGTAACTGATGATACATGATGAATGAATGGTGGGAAGGCACAAGGT	90687
O	y	21241	CTTTGAAGCTGAAACACCTTGATCTTTACCACCCCTTCCTCCTCAGATACTGATATTG	21300
D	b	90688	CTTTGAAGCTGAAACACCTTGATCTTTACCACCCCTTCCTCCTCAGATACTGATATTG	90747
O	y	21301	AGAAATATCCACTATGAATAACCCCTTAGGCCCTGTCTCTATTTCTGGATGAGAAATCCC	21360
D	b	90748	AGAAATATCCACTATGAATAACCCCTTAGGCCCTGTCTCTATTTCTGGATGAGAAATCCC	90807
O	y	21361	TCTCATCTTCTCTGGTCTCTCTCGCTGACACCCCAAGCCCTGGGACCTGGATCTGGCTAC	21420
D	b	90808	TCTCATCTTCTCTGGTCTCTCTCGCTGACACCCCAAGCCCTGGGACCTGGATCTGGCTAC	90867
O	y	21421	TCACCTCTAGCCCTCTCTGGCTCTGCATCTGTCTTTGCCAAGAGCTTACCCGCTCTCCAT	21480
D	b	90868	TCACCTCTAGCCCTCTCTGGCTCTGCATCTGTCTTTGCCAAGAGCTTACCCGCTCTCCAT	90927
O	y	21481	CATTGGGCTTTGATGCGATGGCTTTTGC AAAGCCCTCTCAGGCTGATCTGGCCATCT	21540
D	b	90928	CATTGGGCTTTGATGCGATGGCTTTTGC AAAGCCCTCTCAGGCTGATCTGGCCATCT	90987
O	y	21541	CTGGAGTTTCTGTGCTCTTGCCACTTAAGTTCTCTGGCATATATGGGTAGGTGAACCC	21600
D	b	90988	CTGGAGTTTCTGTGCTCTTGCCACTTAAGTTCTCTGGCATATATGGGTAGGTGAACCC	91047
O	y	21601	AGCCACAGATACCTTTTCACTTTGGGGGTGAATATCTCTGGTCTCCTACTGGAAGAAGC	21660
D	b	91048	AGCCACAGATACCTTTTCACTTTGGGGGTGAATATCTCTGGTCTCCTACTGGAAGAAGC	91107
O	y	21661	CTCTGGCAAATGAATAACAGGCATCTCTATAGCTGCTTTTTTGTCTCTCTGGACATGG	21720
D	b	91108	CTCTGGCAAATGAATAACAGGCATCTCTATAGCTGCTTTTTTGTCTCTCTGGACATGG	91167
O	y	21721	ACATCCCTGCATTTGGAGCTTTTTTTCTTCAGGTTTTCAGCTCTGAAAATTTATGGAGTG	21780
D	b	91168	ACATCCCTGCATTTGGAGCTTTTTTTCTTCAGGTTTTCAGCTCTGAAAATTTATGGAGTG	91227
O	y	21781	ACCAGGACTGCTGTGTGAGCACTGACTCTATTAATATACAGTGTAGAATATTCCATAC	21840
D	b	91228	ACCAGGACTGCTGTGTGAGCACTGACTCTATTAATATACAGTGTAGAATATTCCATAC	91287
O	y	21841	AACACTGCCCTTGATTAACAAACTGGCTACAGGCTGGGTGGTGTTCACGCCCTGTA	21900
D	b	91288	AACACTGCCCTTGATTAACAAACTGGCTACAGGCTGGGTGGTGTTCACGCCCTGTA	91347
O	y	21901	TCCCAACACTTTGGGAGCCGAGGTGGGCAGATCACTTGAGCCCAAGAAATTTGAGACCAG	21960
D	b	91348	TCCCAACACTTTGGGAGCCGAGGTGGGCAGATCACTTGAGCCCAAGAAATTTGAGACCAG	91407
O	y	21961	CTGGGCAACATAGTGAACCCCTGTCTCTATTTAGAAATACAAAAATTTAGCCGCTGACGT	22020
D	b	91408	CTGGGCAACATAGTGAACCCCTGTCTCTATTTAGAAATACAAAAATTTAGCCGCTGACGT	91467
O	y	22021	GCACAGCCTGTAGTCTCAGCTACTCAGGAGGCTGAGGCATGAGAATTCGCTTGATCTGG	22080
D	b	91468	GCACAGCCTGTAGTCTCAGCTACTCAGGAGGCTGAGGCATGAGAATTCGCTTGATCTGG	91527
O	y	22081	GAGGCGGACGTTGCAATGAATGGAGATTGCAACCTGTCTCTCTAGAAATACAAAAATTTAGCCGCTGACGT	22140
D	b	91528	GAGGCGGACGTTGCAATGAATGGAGATTGCAACCTGTCTCTCTAGAAATACAAAAATTTAGCCGCTGACGT	91587
O	y	22141	AAGACTCCCTCTCAGGGAAAAAAGAAAGAGAGAGACTACAATCTGATTTCTTTTAA	22200
D	b	91588	AAGACTCCCTCTCAGGGAAAAAAGAAAGAGAGAGACTACAATCTGATTTCTTTTAA	91647
O	y	22201	ATGAATTCACCTTGACTTAGCAGGTATTGTATTATTAGGAATAACTAGCTTTAGGCCAGG	22260
D	b	91648	ATGAATTCACCTTGACTTAGCAGGTATTGTATTATTAGGAATAACTAGCTTTAGGCCAGG	91707
O	y	22261	TGTGTGGCTCACGCCCTGAATCTCAGCTTTGGGAGGCCAAGGAGGCAGATACCTTG	22320
D	b	91708	TGTGTGGCTCACGCCCTGAATCTCAGCTTTGGGAGGCCAAGGAGGCAGATACCTTG	91767

QY	22321	ATGTCAGAGTTT	TGAGACCAGCTGGTCAACATGGTGAATCTCGCTCTACTTAAATA	22380
DB	91768	ATGTCAGAGTTT	TGAGACCAGCTGGTCAACATGGTGAATCTCGCTCTACTTAAATA	91827
QY	22381	CAACATCTAC	CGAGTGGCGGACCTGTAGTCCAGCTACTCTCAGGAGTTGAGGCAGGA	22440
DB	91828	CAACATCTAC	CGAGTGGCGGACCTGTAGTCCAGCTACTCTCAGGAGTTGAGGCAGGA	91887
QY	22441	GAATTGCTTGA	ACCGAGGTTGATGTAGTGGCCAAAGACTATGCCACTGCACCTCT	22500
DB	91888	GAATTGCTTGA	ACCGAGGTTGATGTAGTGGCCAAAGACTATGCCACTGCACCTCT	91947
QY	22501	AGCCTGGTGAC	AGAGAGACTCCATCTCAAAAAAAAAAAAAAGGAATAACTAG	22560
DB	91948	AGCCTGGTGAC	AGAGAGACTCCATCTCAAAAAAAAAAAAAAGGAATAACTAG	92007
QY	22561	CTTTTTAGAAC	AAATGGAAATGATGACTCAGCTATTCCAGGCTGGGTGCTGCCCTGCAGA	22620
DB	92008	CTTTTTAGAAC	AAATGGAAATGATGACTCAGCTATTCCAGGCTGGGTGCTGCCCTGCAGA	92067
QY	22621	GCAGATATAG	CGCTTATTTTATTTTAAATTTTTTTTTTTTGGACAGGTCCTTACT	22680
DB	92068	GCAGATATAG	CGCTTATTTTATTTTAAATTTTTTTTTTTTGGACAGGTCCTTACT	92127
QY	22681	CTATCGCCCA	GGGTGAGTGCAGTGGCAGCATCTTGGCTCACTGCAATCTCTGCTCTTTG	22740
DB	92128	CTATCGCCCA	GGGTGAGTGCAGTGGCAGCATCTTGGCTCACTGCAATCTCTGCTCTTTG	92187
QY	22741	GGTTCAGCGA	TTCTCTGCTCAGCTCCTGAAATGCTGGGATACAGACGCGCACCAC	22800
DB	92188	GGTTCAGCGA	TTCTCTGCTCAGCTCCTGAAATGCTGGGATACAGACGCGCACCAC	92247
QY	22801	CATGCCCTGT	CTAAATTTTGTATTTTATTTAGTAGAACGGGTTTCATCATGTTGGCCAACT	22860
DB	92248	CATGCCCTGT	CTAAATTTTGTATTTTATTTAGTAGAACGGGTTTCATCATGTTGGCCAACT	92307
QY	22861	TGCTCGAAT	TCCAGCTCAAGTGATCGCTCGCTCGGCCCTCCAAAGTCTGGGAT	22920
DB	92308	TGCTCGAAT	TCCAGCTCAAGTGATCGCTCGCTCGGCCCTCCAAAGTCTGGGAT	92367
QY	22921	ACAGGTGTG	AGGCCACACACAGGCCCAATATAGCTTTAAATCAATGTATATATGCTT	22980
DB	92368	ACAGGTGTG	AGGCCACACACAGGCCCAATATAGCTTTAAATCAATGTATATATGCTT	92427
QY	22981	TGCTCTTTG	GGCCAGAAATGCATAACAGAGAGGTAGCGGTGTGGGCACCTTATAT	23040
DB	92428	TGCTCTTTG	GGCCAGAAATGCATAACAGAGAGGTAGCGGTGTGGGCACCTTATAT	92487
QY	23041	GATTTACCTA	AGGACTTAAGGTTTTCTCTCTCAGATTTCTGGGTATTCAGGTCA	23100
DB	92488	GATTTACCTA	AGGACTTAAGGTTTTCTCTCTCAGATTTCTGGGTATTCAGGTCA	92547
QY	23101	GAAGGTGAT	AGCATCGGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAG	23160
DB	92548	GAAGGTGAT	AGCATCGGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAG	92607
QY	23161	GTCAGCGGG	CGAGATCAATTTAGCTCAGGAATTTGAAATCAGCCTGACCAACATGCTGA	23220
DB	92608	GTCAGCGGG	CGAGATCAATTTAGCTCAGGAATTTGAAATCAGCCTGACCAACATGCTGA	92667
QY	23221	AACCTGTCT	CTACTAAAAATACAAAAATAGCCGGGTGTGGTGGCAGCGCTGTAACT	23280
DB	92668	AACCTGTCT	CTACTAAAAATACAAAAATAGCCGGGTGTGGTGGCAGCGCTGTAACT	92727
QY	23281	CCAGCTACT	CGGGAGCTGAGCAGGAGATGACTTGAACCTGGGAGCGGAGTTGCAG	23340
DB	92728	CCAGCTACT	CGGGAGCTGAGCAGGAGATGACTTGAACCTGGGAGCGGAGTTGCAG	92787
QY	23341	TGAGCTGAG	ATCGGCCACTGCACCTCCAGCTGGTGCACACTGAACTCTGTCTGGGAA	23400
DB	92788	TGAGCTGAG	ATCGGCCACTGCACCTCCAGCTGGTGCACACTGAACTCTGTCTGGGAA	92847

QY	19021	CCAGCTCTCCATTTGAGGCGCTGCTGGACAGACGCCGTTTATACACCCAGCTCCCAAAATC	19080
Db	88468	CCAGCTCTCTCCATTTGAGGCGCTGCTGGACAGACGCCGTTTATATACACCCAGCTCCCAAAATC	88527
QY	19081	CTATTGAGAGCCTCCGCCCTCCGACAGAGCCACCGGCTCCAAACCCCATTTAGAGCTGGCCCTT	19140
Db	88528	CTATTGAGAGCCTCCGCCCTCCGACAGAGCCACCGGCTCCAAACCCCATTTAGAGCTGGCCCTT	88587
QY	19141	TGTCCTGGGGGTTAAAGTGGTTACATGTGTGGGGGACACCCAGAAAGAACGTGCAGAGCTTGG	19200
Db	88588	TGTCCTGGGGGTTAAAGTGGTTACATGTGTGGGGGACACCCAGAAAGAACGTGCAGAGCTTGG	88647
QY	19201	AAAGGCTGTGCTCATATACAGTGGCCCTCCACTAGATGAATGGGGTGGGTGGAGACAGGTGG	19260
Db	88648	AAAGGCTGTGCTCATATACAGTGGCCCTCCACTAGATGAATGGGGTGGGTGGAGACAGGTGG	88707
QY	19261	GCGGCGCCGAGAGGTGGGTGGGGGAGAGGGGCATYGGGGATTTATGAGAGCCACAGAGGACACT	19320
Db	88708	GCGGCGCCGAGAGGTGGGTGGGGGAGAGGGGCATYGGGGATTTATGAGAGCCACAGAGGACACT	88767
QY	19321	GCTAGAGAGGGGGGTGGAAACAGAGCCGCCCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	19380
Db	88768	GCTAGAGAGGGGGGTGGAAACAGAGCCGCCCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	88827
QY	19381	CGCTACCTTACTTCCCTC	19440
Db	88828	CGCTACCTTACTTCCCTC	88887
QY	19441	TTGGCTTTTCTGATGTCTCTGCTGACGCCCTTGATGTGCTGACCTGAGAGAAAGAAATTTATATTA	19500
Db	88888	TTGGCTTTTCTGATGTCTCTGCTGACGCCCTTGATGTGCTGACCTGAGAGAAAGAAATTTATATTA	88947
QY	19501	CCCTTTCATCTTCTCCAGAGCTCCGAAAGAAAGACCTTTCTCCCTCTCTCTCTCTCTCTCTCTCTC	19560
Db	88948	CCCTTTCATCTTCTCCAGAGCTCCGAAAGAAAGACCTTTCTCCCTCTCTCTCTCTCTCTCTCTCTC	89007
QY	19561	GGGTGAGAGGGGGAACAGTCTGGGGGACAGGGGAGCATTCATTTCTCTAGCTTCATCTCG	19620
Db	89008	GGGTGAGAGGGGGAACAGTCTGGGGGACAGGGGAGCATTCATTTCTCTAGCTTCATCTCG	89067
QY	19621	TGCAGTGAATTTGCAGAGCTGTGCCCTGCGCAAACTTTTAAAGCTTCTCTGAAGTTCCCTCG	19680
Db	89068	TGCAGTGAATTTGCAGAGCTGTGCCCTGCGCAAACTTTTAAAGCTTCTCTGAAGTTCCCTCG	89127
QY	19681	GAGCCCTTGGGTGGAGGGTTTACGGGGAAGACAGATCTCAACAGTGGATATATTGGAAAGAT	19740
Db	89128	GAGCCCTTGGGTGGAGGGTTTACGGGGAAGACAGATCTCAACAGTGGATATATTGGAAAGAT	89187
QY	19741	TTTGTGTGAGAAAGAAAGAAATTAATCTTCAAGCGCTCTTAAAGATGCTTTAAACTCTCTAATTGA	19800
Db	89188	TTTGTGTGAGAAAGAAAGAAATTAATCTTCAAGCGCTCTTAAAGATGCTTTAAACTCTCTAATTGA	89247
QY	19801	ATGTACCGGCTGTCAATTTTACAGCTGGGGAACAGCCAAATGGAAGATAGGGGATGG	19860
Db	89248	ATGTACCGGCTGTCAATTTTACAGCTGGGGAACAGCCAAATGGAAGATAGGGGATGG	89307
QY	19861	GCAATATTTTACCTTAAGGTAAACAGATAGTAATTTCTGTATAGCTTAAAGGACACTTTTAC	19920
Db	89308	GCAATATTTTACCTTAAGGTAAACAGATAGTAATTTCTGTATAGCTTAAAGGACACTTTTAC	89367
QY	19921	CTTTAAGAGAGAGTAAAGATAATGATGAACAAACAGTAGTGCATCAGCTTCTCTAGGCC	19980
Db	89368	CTTTAAGAGAGAGTAAAGATAATGATGAACAAACAGTAGTGCATCAGCTTCTCTAGGCC	89427
QY	19981	TTCCCTTTCCAGATGAGAACCATATTTCTGGGAAATATGTTCGTTCATCTGCCCTTAATGG	20040
Db	89428	TTCCCTTTCCAGATGAGAACCATATTTCTGGGAAATATGTTCGTTCATCTGCCCTTAATGG	89487
QY	20041	CTCTTTGGCATGTCAAAAGTCTCTGGGGTTGTGCCTGCTGTTGGAGGCCAAAGTATACAA	20100
Db	89488	CTCTTTGGCATGTCAAAAGTCTCTGGGGTTGTGCCTGCTGTTGGAGGCCAAAGTATACAA	89547
QY	20101	TGTTCCACACATATCTTATTGAAACAATTTTAAAGCATATATATTTTAAAGCCCAAAAAG	20160

Db	89548	TGTTTCACGACATAGTTATTGACAAATTTTCTTAAGGCATATTATTTTATTATACGCCCAAAAAG	89606
Qy	20161	GTTAAAAATGATTTGATTTGCTTAAGTTCCTCAAAAGCATGTGGGAGTTGACAGATGATG	20222
Db	89608	GTTAAAAATATTTGATTTGCTTAAGTTCCTCAAAAGCATGTGGGAGTTGACAGATGATG	89666
Qy	20221	TGACCTCAGAAAGAGAAAGAAAGCAAGGTTTACCAACGTAAGTTGTATATCCAGATCGTGC	20278
Db	89668	TGACCTCAGAAAGAGAAAGAAAGCAAGGTTTACCAACGTAAGTTGTATATCCAGATCGTGC	89722
Qy	20281	TTTGTCTGATATGCAAACTCTGAGGCGTTCCTCAGTTACGTTCCCTGCTGTGCCAGGAT	20344
Db	89728	TTTGTCTGATATGCAAACTCTGAGGCGTTCCTCAGTTACGTTCCCTGCTGTGCCAGGAT	89788
Qy	20341	GGAGGCCAAGCTCCTTGGGATGCTGTCAAGAACTTTCACAACTGGGCCAATTTATCTTC	20400
Db	89788	GGAGGCCAAGCTCCTTGGGATGCTGTCAAGAACTTTCACAACTGGGCCAATTTATCTTC	89844
Qy	20401	TAGCCTACACTTACCTCCATTTTCCACGAGCTCCAGCACACACAGCCCTACGGGGTGTG	20466
Db	89848	TAGCCTACACTTACCTCCATTTTCCACGAGCTCCAGCACACACAGCCCTACGGGGTGTG	89900
Qy	20461	CCGGAACCTACTCTGAAAAATGCAAGTCTCTATGCCCTCTCTGTGCTTCTCTGTGTGAGCT	20522
Db	89908	CCGGAACCTACTCTGAAAAATGCAAGTCTCTATGCCCTCTCTGTGCTTCTCTGTGTGAGCT	89966
Qy	20521	CTTATTCATCCCTCCAAAGGCTTGCTGCAATATACCTCTGTGCTATAGCTGGGTTTATGTGC	20588
Db	89968	CTTATTCATCCCTCCAAAGGCTTGCTGCAATATACCTCTGTGCTATAGCTGGGTTTATGTGC	90022
Qy	20581	TCATGCTCTGTAATCCCAAGATGTTGGAGGCCAAGCTGGAGCATCACTTAAGTTTGGGA	20644
Db	90028	TCATGCTCTGTAATCCCAAGATGTTGGAGGCCAAGCTGGAGCATCACTTAAGTTTGGGA	90088
Qy	20641	GTTTCAGACACACCTTGCGGTAACATGTGCAAGAGCTCCACTCTTAAAAATAAAAAAATCAC	20700
Db	90088	GTTTCAGACACACCTTGCGGTAACATGTGCAAGAGCTCCACTCTTAAAAATAAAAAAATCAC	90144
Qy	20701	CTCTGTGAAGCCTTTCTTACCTTTTCTGAGCTTACTACTTTTGCCTGCTGCTGTT	20766
Db	90148	CTCTGTGAAGCCTTTCTTACCTTTTCTGAGCTTACTACTTTTGCCTGCTGCTGTT	90200
Qy	20761	GCAGGGCCCATTAACATTTGTATAGCCCACTCTGTGCTATCTCTTTTCTTTGAGACAGG	20822
Db	90208	GCAGGGCCCATTAACATTTGTATAGCCCACTCTGTGCTATCTCTTTTCTTTGAGACAGG	90266
Qy	20821	GTCGTGGCTGTGCAACCCAGGCTAGAGTCCGCTGTGTGATCTTGGCTCACATGCACCTCT	20888
Db	90268	GTCGTGGCTGTGCAACCCAGGCTAGAGTCCGCTGTGTGATCTTGGCTCACATGCACCTCT	90322
Qy	20881	GCCTCCCAAGTTCAAGCAGTTCTGTGTGCTCAGGCTCCCAAGTAGCTGGGATTAAGAGCGC	20944
Db	90328	GCCTCCCAAGTTCAAGCAGTTCTGTGTGCTCAGGCTCCCAAGTAGCTGGGATTAAGAGCGC	90388
Qy	20941	TGTGGCACCATATGCCCGGTAAATTTTGTATTTAGTAGAGAGGGGTTTCAACATGTG	21000
Db	90388	TGTGGCACCATATGCCCGGTAAATTTTGTATTTAGTAGAGAGGGGTTTCAACATGTG	90444
Qy	21001	ATCAGGCTGTGTCAAACTCTCTACCTCCACAGTATCTGTCCGCTTCGAGCTCCCAAAAGT	21066
Db	90448	ATCAGGCTGTGTCAAACTCTCTACCTCCACAGTATCTGTCCGCTTCGAGCTCCCAAAAGT	90500
Qy	21061	CTGGAAATTACAGGATATAGCCACACACAGTACTGTGTCTGTCTTCTTCAACAAGAGG	21120
Db	90508	CTGGAAATTACAGGATATAGCCACACACAGTACTGTGTCTGTCTTCTTCTTCAACAAGAGG	90566
Qy	21121	CTGCCCAAGACACAGACAGTCTGTGATTTGTCTGTCAATTTCCCAACACAGTACTGTGGAC	21180
Db	90568	CTGCCCAAGACACAGACAGTCTGTGATTTGTCTGTCAATTTCCCAACACAGTACTGTGGAC	90622
Qy	21181	AAATPAAGCACTCTGTAACTGTATGATACATGTAAATGAATGGGTGGGAAGGACAAAGT	21240

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QY	14641	AGCATATCCGTTTTGTTGAAAAATGTAATGCTTTGGGTAGCACCATGCCGACATATAA	14700
Db	84088	AGCATATCCGTTTTGTTGAAAAATGTAATGCTTTGGGTAGCACCATGCCGACATATAA	84147
QY	14701	TAATTCATATAATTTTTTGAGCAATAGTGAATGGAGGCGCTGGAAAGCTAATGCTGAAA	14760
Db	84148	TAATTCATATAATTTTTTGAGCAATAGTGAATGGAGGCGCTGGAAAGCTAATGCTGAAA	84207
QY	14761	AGCATAGAGCTGAATTTATATACAGAGAGCTTCTAGTCAGAGACAGATATAGAGGTGAG	14820
Db	84208	AGCATAGAGCTGAATTTATATACAGAGAGCTTCTAGTCAGAGACAGATATAGAGGTGAG	84267
QY	14821	AGCTTTAGTCTTGCTCTTTCTCCAGCTGTGAATCATGATGACTTTGGTAAAGTCACT	14880
Db	84268	AGCTTTAGTCTTGCTCTTTCTCCAGCTGTGAATCATGATGACTTTGGTAAAGTCACT	84327
QY	14881	CTTTTTCCTCAACCTGGAAAAATGGGGCTAATGGAATGAAATGCTTGTTAGCTCACAGGT	14940
Db	84328	CTTTTTCCTCAACCTGGAAAAATGGGGCTAATGGAATGAAATGCTTGTTAGCTCACAGGT	84387
QY	14941	ATGGTTAGCATCAAAAGTACAAATTTAATGGAATGAAATGATCATATTTAAGAGCTGCA	15000
Db	84388	ATGGTTAGCATCAAAAGTACAAATTTAATGGAATGAAATGATCATATTTAAGAGCTGCA	84447
QY	15001	CTAATGACAGCTTAACACTACTGCTGAGGAATGGGTAGAGCTGAGTGGGAAGAGACCAA	15060
Db	84448	CTAATGACAGCTTAACACTACTGCTGAGGAATGGGTAGAGCTGAGTGGGAAGAGACCAA	84507
QY	15061	GCCCCAACAAAGGCTCAATGATGTCACATATGGTGGCTAGCTATATGCTGAGACTTGTATA	15120
Db	84508	GCCCCAACAAAGGCTCAATGATGTCACATATGGTGGCTAGCTATATGCTGAGACTTGTATA	84567
QY	15121	GCAGTAGCAAAATGGAGGCGCTGTGTATAGCTCTGAGACTCCAGTAACTGGGAGACATAGAGT	15180
Db	84568	GCAGTAGCAAAATGGAGGCGCTGTGTATAGCTCTGAGACTCCAGTAACTGGGAGACATAGAGT	84627
QY	15181	GCCTTGATGATGGCTGCTGACCTCGAGATTTACCTTTTGAGACCAAGTCCCTGCTTT	15240
Db	84628	GCCTTGATGATGGCTGCTGACCTCGAGATTTACCTTTTGAGACCAAGTCCCTGCTTT	84687
QY	15241	CTGTCCCACTAGTTTATATATGCTTGTCGTACACATCCAGTCCTCCATCCCTCCTTT	15300
Db	84688	CTGTCCCACTAGTTTATATATGCTTGTCGTACACATCCAGTCCTCCATCCCTCCTTT	84747
QY	15301	TTTGTCTCTCTCCTCTCACCTTAAAGGTTTTTCATTTTCACTTTATTGATTAACTTCTA	15360
Db	84748	TTTGTCTCTCTCCTCTCACCTTAAAGGTTTTTCATTTTCACTTTATTGATTAACTTCTA	84807
QY	15361	CCCGTGCTGTGGGATTTCAATATGGGAAAAGGAGTTGAAGTACGTCACAGCTTAAGGGTGA	15420
Db	84808	CCCGTGCTGTGGGATTTCAATATGGGAAAAGGAGTTGAAGTACGTCACAGCTTAAGGGTGA	84867
QY	15421	TTTGAAGAGACTTTGGGCTGGACACTAGTATCCCTCCCTCATTTTATGAGAGAACCTGAGT	15480
Db	84868	TTTGAAGAGACTTTGGGCTGGACACTAGTATCCCTCCCTCATTTTATGAGAGAACCTGAGT	84927
QY	15481	CCGCGGAATTTCTTGATGGCTGTGTGGCTAGATATAGGTTGAAGAGGCAAGCTCCAGCTC	15540
Db	84928	CCGCGGAATTTCTTGATGGCTGTGTGGCTAGATATAGGTTGAAGAGGCAAGCTCCAGCTC	84987
QY	15541	CAGGCTGTGAGAAATTTATGCTAGTCCAAAGGGGTAGAAAAGTGTGAGGCAAGGTTGGAGT	15600
Db	84988	CAGGCTGTGAGAAATTTATGCTAGTCCAAAGGGGTAGAAAAGTGTGAGGCAAGGTTGGAGT	85047
QY	15601	GAGCCGCGTGTGGGTTTTTGGCCCTCATATCTTTTTTTCAGAGGCTGAAGCAAGGAAA	15660
Db	85048	GAGCCGCGTGTGGGTTTTTGGCCCTCATATCTTTTTTTCAGAGGCTGAAGCAAGGAAA	85107
QY	15661	MAAGCTACTGCGCCACACTCTCTGTGTATGCTCTGCTCAATTTAACTTAACTTATTTAT	15720
Db	85108	MAAGCTACTGCGCCACACTCTCTGTGTATGCTCTGCTCAATTTAACTTAACTTATTTAT	85167
QY	15721	CAAAAAGACAGCTTTATTTGGAAAAACAGATGACACTAGGCAAAAAATCATATGCTGTTTTCC	15780

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Db	81868	GCTCAGGCTGGGAGACTTTTTAGGGGGTGTTTTGGTTTTTATCTCCTAGGCTTATGTCT	81921
Qy	12481	AATCACATCTTGTGTGCAATCCCTGCTGGAGTTTGTGCTCCTAAGGATACAGGAGATATTT	12540
Db	81928	AATCACATCTTGTGTGCAATCCCTGCTGGAGTTTGTGCTCCTAAGGATACAGGAGATATTT	81987
Qy	12541	CTGGGAGGAGTGTTCCTCATGATACTATTTGATTTATGTCATCTCTTGAGATGGTATTTGATC	12600
Db	81988	CTGGGAGGAGTGTTCCTCATGATACTATTTGATTTATGTCATCTCTTGAGATGGTATTTGATC	82047
Qy	12601	TTCTACCTCTTATATCCTTACTCATCGCTGSCACACAGCTTGGAAATGTAGTGGCTTACC	12660
Db	82048	TTCTACCTCTTATATCCTTACTCATCGCTGSCACACAGCTTGGAAATGTAGTGGCTTACC	82107
Qy	12661	ACAGTTTGAATAAATAACACTACACCTTTTCAGAGCCTCTGTTTATAAAATGAGGATACTA	12720
Db	82108	ACAGTTTGAATAAATAAACAATACACCTTTTCAGAGCCTCTGTTTATAAAATGAGGATACTA	82167
Qy	12721	AGTCATGGCTGTCTCAGAGTTGCTGGGGGCTTCAGTTTGGAAATGTAGTGGCTTACC	12780
Db	82168	AGTCATGGCTGTCTCAGAGTTGCTGGGGGCTTCAGTTTGGAAATGTAGTGGCTTACC	82227
Qy	12781	ATGTCAAGTCCCACTCTGTAAAGCATAAAGAAATTTGCCAGTAGCTCCCGAGAAAAGAAAT	12840
Db	82228	ATGTCAAGTCCCACTCTGTAAAGCATAAAGAAATTTGCCAGTAGCTCCCGAGAAAAGAAAT	82287
Qy	12841	CACCTCTTTTGAGAAATGAAGAAATTTACCAGTATCACAAATATATCATATATTTGTAGGCC	12900
Db	82288	CACCTCTTTTGAGAAATGAAGAAATTTACCAGTATCACAAATATATCATATATTTGTAGGCC	82347
Qy	12901	ACTTCTGAAAGGCCAATTTCTTCTCAAAATATCTCAAACTTAAATGAAATGTGATCTTC	12960
Db	82348	ACTTCTGAAAGGCCAATTTCTTCTCAAAATATCTCAAACTTAAATGAAATGTGATCTTC	82407
Qy	12961	TCTAAAAACCTGCTCTTCCTCCTGTATTTGCCATTTTCAGTAAAAGTACCTTCCATATATC	13020
Db	82408	TCTAAAAACCTGCTCTTCCTCCTGTATTTGCCATTTTCAGTAAAAGTACCTTCCATATATC	82467
Qy	13021	CAGTCACCTCAGACTGGAAATCTGGAGAGCATTTTGACCTGCTCTTAACTCCTGTAATCA	13080
Db	82468	CAGTCACCTCAGACTGGAAATCTGGAGAGCATTTTGACCTGCTCTTAACTCCTGTAATCA	82527
Qy	13081	GACAATTTCCAAAGTCTGTATTTCTACTCTTCCAAATTCGATCTGGAAATCAGCTCATTTCT	13140
Db	82528	GACAATTTCCAAAGTCTGTATTTCTACTCTTCCAAATTTGCAATTCGAAATCAGCTCATTTCT	82587
Qy	13141	TCCAGCTCTATGCGCAGCCCTCTGTCCAAAGATTCACAAATTTCTTCTTAGGGCTCTACC	13200
Db	82588	TCCAGCTCTATGCGCAGCCCTCTGTCCAAAGATTCACAAATTTCTTCTTAGGGCTCTACC	82647
Qy	13201	GTAGCTCTCTGACCCCCCCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	13260
Db	82648	GTAGCTCTCTGACCCCCCCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	82707
Qy	13261	CCAGAGGCGACCTTTATGTAATATAATTTTGAGAGATGACACTTCACTACTTAAATCTTT	13320
Db	82708	CCAGAGGCGACCTTTATGTAATATAATTTTGAGAGATGACACTTCACTACTTAAATCTTT	82767
Qy	13321	TTTAAATGCTTCCGCTGCACTCAAAAGTTTCAACTTCTCATGGCCGATGCATGACATAGCTC	13380
Db	82768	TTTAAATGCTTCCGCTGCACTCAAAAGTTTCAAACTTCTCATGGCCGATGCATGACATAGCTC	82827
Qy	13381	TGCCCTCCAAACCTGCTGTCTACTCTCTTCTCATGACATGACGCTCAGGAGCATCTTAA	13440
Db	82828	TGCCCTCCAAACCTGCTGTCTACTCTTCTTCTCATGACATGACGCTCAGGAGCATCTTAA	82887
Qy	13441	AGTGTCTCTTTCCCTGGAAATGCCCTCCCTACATCCATCCTCTTCTTGTCTGACTTAA	13500
Db	82888	AGTGTCTCTTTTCCCTGGAAATGCCCTCCCTACATCCATCCTCTTCTTGTCTGACTTAA	82947
Qy	13501	TGCATAATTTCTCAAGGTGTAGCTTAAAGCCTTAATTTTCTCAGAGAGCCTTCTCTGACCA	13560
Db	82948	TGCATAATTTCTCAAGGTGTAGCTTAAAGCCTTAATTTTCTCAGAGAGCCTTCTCTGACCA	83007

[illegible]

QY	10261	CTCCACCTAAATTTTGTATTTTATTTATTTAGAGATAGGTTTGCACATGTGGCCAGGCTG	10320
Db	79708	CTCCACCTAAATTTTGTATTTTATTTATTTAGAGATAGGTTTGCACATGTGGCCAGGCTG	79767
QY	10321	GCTCTGAATCCTTACCTGAGAGTATCCACCCTGTGGCCTCCCAAAAGCTGGGATTA	10380
Db	79768	GCTCTGAATCCTTACCTGAGAGTATCCACCCTGTGGCCTCCCAAAAGCTGGGATTA	79827
QY	10381	TAGGATGAGGCACACGACCCGGCGGTTTCTACAGTTTCTAATACTCAAGATGTGA	10440
Db	79828	TAGGATGAGGCACACGACCCGGCGGTTTCTACAGTTTCTAATACTCAAGATGTGA	79887
QY	10441	CTTTGCAAACTACTATGTGTGTATACCTGTATACCTTAAATGCGGAAAATGTGATAAG	10500
Db	79888	CTTTGCAAACTACTATGTGTGTATACCTGTATACCTTAAATGCGGAAAATGTGATAAG	79947
QY	10501	ATGTTTAAATATGATGTAGTTTTCATAAATCTTAAATGCTGAAGGAAAGATTTGCT	10560
Db	79948	ATGTTTAAATATGATGTAGTTTTCATAAATCTTAAATGCTGAAGGAAAGATTTGCT	80007
QY	10561	GTCACGCTTAAATGCTATCTTGTGGTCACTGCTGTCTAACCTTGAGGACATTTCAAT	10620
Db	80008	GTCACGCTTAAATGCTATCTTGTGGTCACTGCTGTCTAACCTTGAGGACATTTCAAT	80067
QY	10621	TTGAGGTTATCTCCATCCACGAGAAACCTCTGGGTCTAAACATGAGAAGCTGCGCAAT	10680
Db	80068	TTGAGGTTATCTCCATCCACGAGAAACCTCTGGGTCTAAACATGAGAAGCTGCGCAAT	80127
QY	10681	GTCGCTCACTGCTCTTCACTGCTAGTGAATGTATCAAGTAACTTACCAAGTGGTTTG	10740
Db	80128	GTCGCTCACTGCTCTTCACTGCTAGTGAATGTATCAAGTAACTTACCAAGTGGTTTG	80187
QY	10741	GGTTCAAGCTCAGGTGAAGAGGATTAATGATTAATCAATTAATGTAATGTAATGTAATGCT	10800
Db	80188	GGTTCAAGCTCAGGTGAAGAGGATTAATGATTAATCAATTAATGTAATGTAATGTAATGCT	80247
QY	10801	CTTTGTTTAAAAAAGCTTATTTTTTAAAGACAGTCCTCTGTTGCCAGTTTAGAGTGC	10860
Db	80248	CTTTGTTTAAAAAAGCTTATTTTTTAAAGACAGTCCTCTGTTGCCAGTTTAGAGTGC	80307
QY	10861	AGTGCACATATCTACTCACTGACCTGGAAGTCTCTGGGCTTCAAGCATCTCTTCTCT	10920
Db	80308	AGTGCACATATCTACTCACTGACCTGGAAGTCTCTGGGCTTCAAGCATCTCTTCTCT	80367
QY	10921	CAACCTTGGAAATAGCTGGGCCACATTAACAGGCATATGCCACCATGCGCAGTAAATT	10980
Db	80368	CAACCTTGGAAATAGCTGGGCCACATTAACAGGCATATGCCACCATGCGCAGTAAATT	80427
QY	10981	TATTTTATAGAGACAGGCTCTGTGCTGTGCTCCAGCTGATCTTGAATCCTGTGCT	11040
Db	80428	TATTTTATAGAGACAGGCTCTGTGCTGTGCTCCAGCTGATCTTGAATCCTGTGCT	80487
QY	11041	CAAGTAATCTCCCACTTGGCTTCCCAAAATGCTGGGTCAAGGCTCAGCCACCATGC	11100
Db	80488	CAAGTAATCTCCCACTTGGCTTCCCAAAATGCTGGGTCAAGGCTCAGCCACCATGC	80547
QY	11101	CCAGCTGTTAAGGCTTGTATGAGCTTCTCTTGAAGTATGTTGTATGTAATCTTATTT	11160
Db	80548	CCAGCTGTTAAGGCTTGTATGAGCTTCTCTTGAAGTATGTTGTATGTAATCTTATTT	80607
QY	11161	TATTCATGGGTTCAAGATACATGTTTTTCCCTTCTTTGAAGCTCTTAACAGTTGCC	11220
Db	80608	TATTCATGGGTTCAAGATACATGTTTTTCCCTTCTTTGAAGCTCTTAACAGTTGCC	80667
QY	11221	AAGGAAAGTACCCCTTGTGGGCAAAAGAACTGAGAGGAAAGGCTAGATATTTCTTC	11280
Db	80668	AAGGAAAGTACCCCTTGTGGGCAAAAGAACTGAGAGGAAAGGCTAGATATTTCTTC	80727
QY	11281	CCTCTTGTTCCTTACATGCTCTTTGAGAGAGATAGAAAGCAATTTGAATTTGCAAC	11340
Db	80728	CCTCTTGTTCCTTACATGCTCTTTGAGAGAGATAGAAAGCAATTTGAATTTGCAAC	80787
QY	11341	TGAGGATTAAGAAATTCACCCAGGTCGGTGCCTCAGCCACACATTTTAGGAGACTGAGG	11400

Db	80788	TGAGGATTAAGAAAAATTCACCCAGGCTCCGGTGGCTACACCCAGCACTTTAGAGACTGAGC	11466
OY	11401	TGGGTGCATTGGTTGAACCTCAGAGATTGAGAACCCAGCCTTGGGAAACATGGTGAATCCCA	11466
Db	80848	TGGGTGCATTGGTTGTAACCTCAGAGATTGAGAACCCAGCCTTGGGAAACATGGTGAATCCCA	80907
OY	11461	ACCTTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAATTAAGTCCCTGAGAAAATCCAGGC	11520
Db	80908	ACCTTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAATTAAGTCCCTGAGAAAATCCAGGC	80967
OY	11521	AGAAAATGGTTCTTGGGCTGGGCGGTGGTATGGCTGTAATCTGAGCACTTTGGGAG	11586
Db	80968	AGAAAATGGTTCTTGGGCTGGGCGGTGGTATGGCTGTAATCTGAGCACTTTGGGAG	81027
OY	11581	GCTGAGGCAAGCTGGATACCTTAAGTCCAGAGTTGGAGACCAGACTGACCAACAGGTGA	11644
Db	81028	GCTGAGGCAAGCTGGATACCTTAAGTCCAGAGTTGGAGACCAGACTGACCAACAGGTGA	81087
OY	11641	AACCCCGTCTACCTTAATAACAAAAATGACGAGCTTGGTGGTGGCAGTGGCTCTGA	11700
Db	81088	AACCCCGTCTACCTTAATAACAAAAATGACGAGCTTGGTGGTGGCAGTGGCTCTGA	81144
OY	11701	GTCCCAAGCTACTTGGGAGGCTTGAGACAAGAAATGGCTTGAACCTTGAGAGCAGAGTTG	11767
Db	81148	GTCCCAAGCTACTTGGGAGGCTTGAGACAAGAAATGGCTTGAACCTTGAGAGCAGAGTTG	81207
OY	11761	CAGTAGCCGAGATATAGCCCACTGCTCCAGCATGGGCCACAGATGAGACTCCCTCTC	11820
Db	81208	CAGTAGCCGAGATATAGCCCACTGCTCCAGCATGGGCCACAGATGAGACTCCCTCTC	81267
OY	11821	AAAAAAAAAAAAAAAAAGAAAAGAAAATGGTTTCTGATTGAGGCTCCTGGAGAAAAGCACTCTC	11880
Db	81268	AAAAAAAAAAAAAAAAAGAAAAGAAAATGGTTTCTGATTGAGGCTCCTGGAGAAAAGCACTCTC	81327
OY	11881	TTGGGAAAGAAAACTTGAGTCAAACTCTGGGTTACTTTCTTATCCAGAGATGGCTCG	11940
Db	81328	TTGGGAAAGAAAACTTGAGTCAAACTCTGGGTTACTTTCTTATCCAGAGATGGCTCG	81387
OY	11941	TATAAAGTAAAGCTAAGGCTTGATCTTGGTAAACAGAGATTGACATGAGCAAGTTCAATCTGA	12000
Db	81388	TATAAAGTAAAGCTAAGGCTTGATCTTGGTAAACAGAGATTGACATGAGCAAGTTCAATCTGA	81447
OY	12001	CCCATATGCCCTTTGGCCCAAGCACTGACGACGACGACATCAGTTATCTTTAATGAAAT	12060
Db	81448	CCCATATGCCCTTTGGCCCAAGCACTGACGACGACGACATCAGTTATCTTTAATGAAAT	81507
OY	12061	GAAGCCCGAGACCTGCGACATATGCGCTGAGGAGAGCTCAGTACATAGCTTGAAT	12120
Db	81508	GAAGCCCGAGACCTGCGACATATGCGCTGAGGAGAGCTCAGTACATAGCTTGAAT	81567
OY	12121	TACATATTTGGAGGAGTGAAGCCCATAGTGTGGAGAGTAGGCTAGGCTCAGTGTCACT	12180
Db	81568	TACATATTTGGAGGAGTGAAGCCCATAGTGTGGAGAGTAGGCTAGGCTCAGTGTCACT	81627
OY	12181	GTTTTTGTTCCTCTGTTCCATACACTGATTAAGGATTAACATGGTATTAACTCTCTTA	12240
Db	81628	GTTTTTGTTCCTCTGTTCCATACACTGATTAAGGATTAACATGGTATTAACTCTCTTA	81687
OY	12241	AACAGGTCTCTAATTTCACTCATTAATTAACAGTTGACAGCCATACAGGCTCTCTTC	12300
Db	81688	AACAGGTCTCTAATTTCACTCATTAATTAACAGTTGACAGCCATACAGGCTCTCTTC	81747
OY	12301	CATAAACCAATAAATTTATATCCACAAAGCTTGAAGACAGGTAAGTACATCTCTGGG	12360
Db	81748	CATAAACCAATAAATTTATATCCACAAAGCTTGAAGACAGGTAAGTACATCTCTGGG	81807
OY	12361	CATCCCTCATTTTCTCAACTGCTTCTCAACAACTCTCTCAGTTTGAAGTTCTAAT	12420
Db	81808	CATCCCTCATTTTCTCAACTGCTTCTCAACAACTCTCTCAGTTTGAAGTTCTAAT	81867
OY	12421	GCTAGGCTGGAGACTTTTAAAGGCGGTGTTTTGTTTTTAATCTCAAGGTTATGCT	12480

Db	76408	ACAGGTACTTAGATCTAGACTAATGGCGAGTAGACACTGATATCTAGATATATGTGG	76467
OY	7021	CTGGTTTACTTTATGTTCTTAAGGCTCAGACTAGTTAATTCGCTTCTCTAGTGGCC	7080
Db	76468	CTGGTTTTACTTTATGTTCTTAAGGCTCAGACTAGTTAATTCGCTTCTCTAGTGGCC	76527
OY	7081	ACGATTGTATACCTAAGTGTAGAGGTAGAGGTTGGAATCCAGAAATTTTAACTCCAGAA	7140
Db	76528	AGGATTGTATACCTAAGTGTAGAGGTTGGAATCCAGAAATTTTAACTCCAGAA	76587
OY	7141	ATGAAGCTCTTCACATTTCCCTACACTGACACTCTCTTTTCTTAAATGATTACTGT	7200
Db	76588	ATGAAGCTCTTCACATTTCCCTACACTGACACTCTCTTTTCTTAAATGATTACTGT	76647
OY	7201	CACATAGTTGGTCTCTTCTTGGAGCCATTTATAGTTGAAGTACCATTTATATA	7260
Db	76648	CACATAGTTGGTCTCTTCTTGGAGCCATTTATAGTTGAAGTACCATTTATATA	76707
OY	7261	GAAACAGTCCCATGAGCTTACGATATGTAGTTAGTTACAAATTTCTTACTTGTTTA	7320
Db	76708	GAAACAGTCCCATGAGCTTACGATATGTAGTTAGTTAGTTACAAATTTCTTACTTGTTTA	76767
OY	7321	GATTTAAAGTATTTCTATAGCTTTTCCACAAATAGGCTCTGTCTTTCTTTTCCA	7380
Db	76768	GATTTAAAGTATTTCTATAGCTTTTCCACAAATAGGCTCTGTCTTTCTTTTCCA	76827
OY	7381	GCCAGTCGCCCTATAGTGTATTCAGAGATCCAAAGCTTGTGTCGAATCCCTTTGAAGC	7440
Db	76828	GCCAGTCGCCCTATAGTGTATTCAGAGATCCAAAGCTTGTGTCGAATCCCTTTGAAGC	76887
OY	7441	ATCAGACACGAGTGTCTCAACAGGTGTGTGGGAACCTGTTAATCTGACATCTATGTC	7500
Db	76888	ATCAGACACGAGTGTCTCAACAGGTGTGTGGGAACCTGTTAATCTGACATCTATGTC	76947
OY	7501	TACAGGTTATTAAGGCCAGTCCAGCTTGAAGAATAGTCTGTCTATTAGAGGAAGAG	7560
Db	76948	TACAGGTTATTAAGGCCAGTCCAGCTTGAAGAATAGTCTGTCTATTAGAGGAAGAG	77007
OY	7561	GTGGCTGAGGAAAAAGTTAATGTCAAAGAGTGTCTATTCTTTCTATTGATAG	7620
Db	77008	GTGGCTGAGGAAAAAGTTAATGTCAAAGAGTGTCTATTCTTTCTATTGATAG	77067
OY	7621	GGTAGGCATATGTACCCCTCAATATCTAGGGGGAAGCAGGAGGAAAGCACTTTCAATCT	7680
Db	77068	GGTAGGCATATGTACCCCTCAATATCTAGGGGGAAGCAGGAGGAAAGCACTTTCAATCT	77127
OY	7681	TTAGTTGGCACTTGGATTGTATACAGATGACTCTTCTCTGAGGGAAGACAGGCT	7740
Db	77128	TTAGTTGGCACTTGGATTGTATACAGATGACTCTTCTCTGAGGGAAGACAGGCT	77187
OY	7741	CACGTCCTAAACCAAGCCCAAAGCTGTGCTCAGAAACTGGCTCTCTCTGACATAAC	7800
Db	77188	CACGTCCTAAACCAAGCCCAAAGCTGTGCTCAGAAACTGGCTCTCTCTGACATAAC	77247
OY	7801	CCAGTGTCTCTCGAAATTCAGAAACTTGTCTTTTATACATCTTCTCTCTGCAAGCTG	7860
Db	77248	CCAGTGTCTCTCGAAATTCAGAAACTTGTCTTTTATACATCTTCTCTCTGCAAGCTG	77307
OY	7861	AGGCGGCAAAAGAAATGCTTAAGTCTCAGGTAATGCAATTTGAAATTAATGTGGCTT	7920
Db	77308	AGGCGGCAAAAGAAATGCTTAAGTCTCAGGTAATGCAATTTGAAATTAATGTGGCTT	77367
OY	7921	CCCAAAACCAAAATTTATCTATTATTTAAATTTAAAAACAAAATTCGCTTAACCTCT	7980
Db	77368	CCCAAAACCAAAATTTATCTATTATTTAAATTTAAAAACAAAATTCGCTTAACCTCT	77427
OY	7981	ATGCTGCAGTGTGAATCTTGTGACCTCCCGATAAGGTACAGAGAAATTCCTACCCAGT	8040
Db	77428	ATGCTGCAGTGTGAATCTTGTGACCTCCCGATAAGGTACAGAGAAATTCCTACCCAGT	77487
OY	8041	CGGTAATCACTTTTAACTGCGGAGAAAGTTTATCTTCTCTTTTCTCTGTTCT	8100

Db	73108	AACATTTTCTATGATGTTAAAGAAAGTTTATATAGATAAATCTTAATAGATTAATA	73167
QY	3721	TTATATGTATGATGATTTGGAATTCACATATAGGACATCATATGATCCCTATTAG	3780
Db	73168	TTATATGTATGATGATTTGGAATTCACATATAGGACATCATATGATCCCTATTAG	73227
QY	3781	ATTATATGTTGCTTTTATCCCATCATTTTCAATTAAGATTCACATTTGGGTTCTAA	3840
Db	73228	ATTATATGTTGCTTTTATCCCATCATTTTCAATTAAGATTCACATTTGGGTTCTAA	73287
QY	3841	TTTATACCTATCAAAATTAACCTCTACACAGCTTTTAGGTTATCCATAGATTTTCTAAGG	3900
Db	73288	TTTATACCTATCAAAATTAACCTCTACACAGCTTTTAGGTTATCCATAGATTTTCTAAGG	73347
QY	3901	TAGTGGTTCTTCTCTCAGAGCTTTTGTTCAAATAAATCTTTTAAAGAAATACAGATA	3960
Db	73348	TAGTGGTTCTTCTCTCAGAGCTTTTGTTCAAATAAATCTTTTAAAGAAATACAGATA	73407
QY	3961	AAAGTTGAAGTCTCAAGATGTAAGTGGGAAGTTTGGGAACTTAGTGACTAGTGGCC	4020
Db	73408	AAAGTTGAAGTCTCAAGATGTAAGTGGGAAGTTTGGGAACTTAGTGACTAGTGGCC	73467
QY	4021	TCTGAAGGAATTTTCCAGGAAGTCTAGGATTTAGAACAACTTAGTCTTAAAGAAATACAG	4080
Db	73468	TCTGAAGGAATTTTCCAGGAAGTCTAGGATTTAGAACAACTTAGTCTTAAAGAAATACAG	73527
QY	4081	TATAGGCTGGGCTGGCTCATGCTCTTAATCCAGCACCTTTGGGAGGCTGAGATGGA	4140
Db	73528	TATAGGCTGGGCTGGCTCATGCTCTTAATCCAGCACCTTTGGGAGGCTGAGATGGA	73587
QY	4141	CAGATCCCTGAGGTCAGAGTTCAAGACAGCCCTGGCCAACTGGTGAACCCCTATCTC	4200
Db	73588	CAGATCCCTGAGGTCAGAGTTCAAGACAGCCCTGGCCAACTGGTGAACCCCTATCTC	73647
QY	4201	TACTAAAAAACAATAATAGCCAGCATGTTGGCAGCCACCTGTAATCCCACTACTCG	4260
Db	73648	TACTAAAAAACAATAATAGCCAGCATGTTGGCAGCCACCTGTAATCCCACTACTCG	73707
QY	4261	GGAGGTTGAGGCATGAGATCACTTGAACCCAGGAGTGGAGGTTGCACTGAGCCGAGAT	4320
Db	73708	GGAGGTTGAGGCATGAGATCACTTGAACCCAGGAGTGGAGGTTGCACTGAGCCGAGAT	73767
QY	4321	GCATCTCTGCACTCCAGCTAGGCGACAGAGGACCTTCACTCAAAAAAATAAAAA	4380
Db	73768	GCATCTCTGCACTCCAGCTAGGCGACAGAGGACCTTCACTCAAAAAAATAAAAA	73827
QY	4381	AGAGAAATPACAGTATAGTCTTCGATAAAATCAGTTTTCAGAAAGCCCAACTTCT	4440
Db	73828	AGAGAAATPACAGTATAGTCTTCGATAAAATCAGTTTTCAGAAAGCCCAACTTCT	73887
QY	4441	GCATTTTGGACCAATGGGACCAAGGTGACTTTTGAATCCAGGTTGACACAGATTTATT	4500
Db	73888	GCATTTTGGACCAATGGGACCAAGGTGACTTTTGAATCCAGGTTGACACAGATTTATT	73947
QY	4501	CTCCGGGGAGCTGAAGTCATAGAAAGTAACTAGTGGTTTGAATACAGAGCTCTGAG	4560
Db	73948	CTCCGGGGAGCTGAAGTCATAGAAAGTAACTAGTGGTTTGAATACAGAGCTCTGAG	74007
QY	4561	CCTTAGTCTCTCTCTGATGTGGGGTCAAGATTTGTTAGGCTGTAAAGATCCCACTT	4620
Db	74008	CCTTAGTCTCTCTCTGATGTGGGGTCAAGATTTGTTAGGCTGTAAAGATCCCACTT	74067
QY	4621	TATTACCTTTCTACACCAACCATCTCTAGTTTGTCTTTAAAGCTGTGTCTCAAAATG	4680
Db	74068	TATTACCTTTCTACACCAACCATCTCTAGTTTGTCTTTAAAGCTGTGTCTCAAAATG	74127
QY	4681	CAAAATGAATAGTTTGAACCTTCCAGCAGGATTTCTAATACATGTAAGAGATTAAGA	4740
Db	74128	CAAAATGAATAGTTTGAACCTTCCAGCAGGATTTCTAATACATGTAAGAGATTAAGA	74187
QY	4741	CTTTTCTGGCTTTCAAAATCACCAATCTAAGTCTGAATCCAGGCTCTGCTACTCTAGCT	4800
Db	74188	CTTTTCTGGCTTTCAAAATCACCAATCTAAGTCTGAATCCAGGCTCTGCTACTCTAGCT	74247
QY	4801	ATCTGACCTTGGGTAATGTAAATCTTCTGAGGCTCAATTCCTCACTGTAATAATGAAG	4860
Db	74248	ATCTGACCTTGGGTAATGTAAATCTTCTGAGGCTCAATTCCTCACTGTAATAATGAAG	74307
QY	4861	AGAATAATAGTACCCATCTCTATGATAATATGTAATGCTGTAAAGCAGCTTATTAGC	4920
Db	74308	AGAATAATAGTACCCATCTCTATGATAATATGTAATGCTGTAAAGCAGCTTATTAGC	74367
QY	4921	ACACAAGACATATTAAGTGATCAACCTTTTAAATACAGATGCTCCACATCTTACATTAAC	4980
Db	74368	ACACAAGACATATTAAGTGATCAACCTTTTAAATACAGATGCTCCACATCTTACATTAAC	74427
QY	4981	CTATATCTCTGATCAATCCATCATAGTTCGAAATGCACCTTCATATTTCCAGATATAAC	5040
Db	74428	CTATATCTCTGATCAATCCATCATAGTTCGAAATGCACCTTCATATTTCCAGATATAAC	74487
QY	5041	TCATGCTAAATCGAAGACATATAAGTGCCTATCACATTCATGTCATCGTAAGATTGA	5100
Db	74488	TCATGCTAAATCGAAGACATATAAGTGCCTATCACATTCATGTCATCGTAAGATTGA	74547
QY	5101	AAAATCATTAAGTCAAAACCATCATAGTGCAGACATTAACAAAAATTTAAATATTATC	5160
Db	74548	AAAATCATTAAGTCAAAACCATCATAGTGCAGACATTAACAAAAATTTAAATATTATC	74607
QY	5161	AAATGTATTATTATTATTATTAGAGTGACTCTGTTCTGCTTTTCTTCTGCTCCATA	5220
Db	74608	AAATGTATTATTATTATTATTAGAGTGACTCTGTTCTGCTTTTCTTCTGCTCCATA	74667
QY	5221	TTCTGTGAGTATATTCAITGTTGCAATTTCTAATCCTCAAAATTCCTTCTAGGAGTTG	5280
Db	74668	TTCTGTGAGTATATTCAITGTTGCAATTTCTAATCCTCAAAATTCCTTCTAGGAGTTG	74727
QY	5281	AGGAAATACCTCGAGGATGAGCAGAGTGTGAGGAAGTGTGGGAGGGAAGATGAG	5340
Db	74728	AGGAAATACCTCGAGGATGAGCAGAGTGTGAGGAAGTGTGGGAGGGAAGATGAG	74787
QY	5341	TATGATGGGGAAGAAATTTGATGAATATGAAGAGGACGTAATGATGAAGTACTTCTTCT	5400
Db	74788	TATGATGGGGAAGAAATTTGATGAATATGAAGAGGACGTAATGATGAAGTACTTCTTCT	74847
QY	5401	GATGAGGAATTCAGAGTCAAAATCAAGAAAAATACACATGTCAGTATCCCAATAGCCCTT	5460
Db	74848	GATGAGGAATTCAGAGTCAAAATCAAGAAAAATACACATGTCAGTATCCCAATAGCCCTT	74907
QY	5461	CTGAGTAATAGGGTACATCTTAAAGCAAGCCCTGTAAACCCAGCAATGGTCTTCTTCT	5520
Db	74908	CTGAGTAATAGGGTACATCTTAAAGCAAGCCCTGTAAACCCAGCAATGGTCTTCTTCT	74967
QY	5521	GAACACCTTATTTCTCTGTTGAGGAAACATATGTTGGATGATGAAGCAGACGCTAC	5580
Db	74968	GAACACCTTATTTCTCTGTTGAGGAAACATATGTTGGATGATGAAGCAGACGCTAC	75027
QY	5581	GTTTATACCAAGAGAGTACCTTCTGATGGGATCTGCACAGCGATGGTCTTGGGGAA	5640
Db	75028	GTTTATACCAAGAGAGTACCTTCTGATGGGATCTGCACAGCGATGGTCTTGGGGAA	75087
QY	5641	TGAGGAAGTTTCGATGGGAAACATAGTATCTTGGTGTGTTGCTTTTAAAGCAATCAGT	5700
Db	75088	TGAGGAAGTTTCGATGGGAAACATAGTATCTTGGTGTGTTGCTTTTAAAGCAATCAGT	75147
QY	5701	TACGGGCTGAGCATGGTGGCTCAGGCTGTAAATCCCAACTTTTGGGAGGAGGAGGAGG	5760
Db	75148	TACGGGCTGAGCATGGTGGCTCAGGCTGTAAATCCCAACTTTTGGGAGGAGGAGGAGG	75207
QY	5761	TGATCAAGAGGTCAGGAGTTCAGGACCCAGCTGACAAATGTTGTAACCCCTGCTTA	5820
Db	75208	TGATCAAGAGGTCAGGAGTTCAGGACCCAGCTGACAAATGTTGTAACCCCTGCTTA	75267
QY	5821	CTAAAGTTTCAAAATTTAGCAGGCTGTGATGGCAGCGCTGTAAATCCCACTACTCAGG	5880
Db	75268	CTAAAGTTTCAAAATTTAGCAGGCTGTGATGGCAGCGCTGTAAATCCCACTACTCAGG	75327

Db	72028	TTAAATAGTTGGCACATTTTAACTAAATCTCCTGGCTCAGCTTCCAAAGTAGCTGGGA	72087
OY	2641	CAACAGGCATGTCGCCACCAACACCTGGCTAAATCTTTCTATTTTGTAGAGATGGGGCT	2700
Db	72088	CAACAGGCATGTGCCACCAACCTGGCTAAATCTTTCTATTTTGTAGAGATGGGGCT	72147
OY	2701	TGCTTGTGCCAGGCTGTCTTAAACGTGTGGCTTAATGATCCCTGCTGTCTT	2760
Db	72148	TGCTTGTGCCAGGCTGTCTTAAACGTGTGGCTTAATGATCCCTGCTGTCTT	72207
OY	2761	CCCAAGTCTGGGATTACAGGCATGAGCCACACAGGCCACCTTTTGTGTGTGTGT	2820
Db	72208	CCCAAGTCTGGGATTACAGGCATGAGCCACACAGGCCACCTTTTGTGTGTGTGT	72267
OY	2821	TTTTTTTGAAGGAGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2880
Db	72268	TTTTTTTGAAGGAGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	72327
OY	2881	GGCTACATGCAACCTCCGCTCCGGGTTAAAGCCATTCTGTGTGTGTGTGTGTGT	2940
Db	72328	GGCTACATGCAACCTCCGCTCCGGGTTAAAGCCATTCTGTGTGTGTGTGTGTGT	72387
OY	2941	TGCTGGGAAATTAAGCACCTGTGCCACACACCCAGCTAAATTTTGTATTTAGTAGA	3000
Db	72388	TGCTGGGAAATTAAGCACCTGTGCCACACACCCAGCTAAATTTTGTATTTAGTAGA	72447
OY	3001	CGGGTTTTACCATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3060
Db	72448	CGGGTTTTACCATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	72507
OY	3061	TTGGGCTTCCAAATGCTGGGATTACAGGCTGAGCCACCCACCTGGGCGCCCAATC	3120
Db	72508	TTGGGCTTCCAAATGCTGGGATTACAGGCTGAGCCACCCACCTGGGCGCCCAATC	72567
OY	3121	ATTTTGTGATATCTGTCTGTGGCATGAAGTAAATTTTATTTTATAGATATTTAAA	3180
Db	72568	ATTTTGTGATATCTGTCTGTGGCATGAAGTAAATTTTATTTTATAGATATTTAAA	72627
OY	3181	CAATCAACATGGGTGTCAGTGGCCACGCCCTATMATCTCAGCATTTGGGAAGCTGAGC	3240
Db	72628	CAATCAACATGGGTGTCAGTGGCCACGCCCTATMATCTCAGCATTTGGGAAGCTGAGC	72687
OY	3241	GGGTGATCATCTGAGTCAAGGATTGAGAGCCACCTGCGCCACATGCGCAGACCCCT	3300
Db	72688	GGGTGATCATCTGAGTCAAGGATTGAGAGCCACCTGCGCCACATGCGCAGACCCCT	72747
OY	3301	CTTACTAAAAATACAAATTTAGCCAAAGGTGTGATGGCTGTGTAATCCAGCTACT	3360
Db	72748	CTTACTAAAAATACAAATTTAGCCAAAGGTGTGATGGCTGTGTAATCCAGCTACT	72807
OY	3361	CAGAGGCAAAAGCTGGGAAATGCTTTGAACCGGAGGTGAGAGGTGACAGCTGAGAT	3420
Db	72808	CAGAGGCAAAAGCTGGGAAATGCTTTGAACCGGAGGTGAGAGGTGACAGCTGAGAT	72867
OY	3421	TGTGCCATTCATTCAGCTCGGCGACGAGAAATCCCATCTCCCGGACCCCGCAA	3480
Db	72868	TGTGCCATTCATTCAGCTCGGCGACGAGAAATCCCATCTCCCGGACCCCGCAA	72927
OY	3481	AAAAAGAAATCAGAAAGATATAAATTAACCTTATCCATGTCCACCATCCAGGATATAA	3540
Db	72928	AAAAAGAAATCAGAAAGATATAAATTAACCTTATCCATGTCCACCATCCAGGATATAA	72987
OY	3541	TGAAGTTACTTTGTCCCTTAATCTTTTATGCAATATTTTATATATGTTGACATT	3600
Db	72988	TGAAGTTACTTTGTCCCTTAATCTTTTATGCAATATTTTATATATGTTGACATT	73047
OY	3601	TGTACAATCTTCTATATGATATTAATTTGCACTTTTGTCTACTAGCATATCCAGA	3660
Db	73048	TGTACAATCTTCTATATGATATTAATTTGCACTTTTGTCTACTAGCATATCCAGA	73107
OY	3661	AACATTTCTATGATGTTAAAAAGTTTATAAGATAATCTAATAGTATTTAATA	3720

AUTHORS Howden, P.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT

On Sep 19, 2000 this sequence version replaced g1:9714820.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 1 constructed by the Sanger Centre Chromosome 1 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
 This sequence is the entire insert of clone RP11-43507 The true
 left end of clone RP1-6283 is at 123829 in this sequence. The true
 right end of clone RP4-555P23 is at 81044 in this sequence. This
 sequence has been finished according to sequence map criteria as
 follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated repeat sequence elements. Where the sequence is
 ambiguous, there is an annotation using the 'unsure' feature key.
 RP11-43507 is from the library RPCR-11.2 constructed by the group
 of Pister de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6

FEATURES

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repeat_region	2010..2057
	/note="24 copies 2 mer tt 75% conserved"
repeat_region	2353..2650
	/note="AluSg1 repeat: matches 1..301 of consensus"
misc_feature	5390..6351
	/note="CpG island"
	/evidence=not_experimental
repeat_region	7263..7656
	/note="MIRB repeat: matches 1..390 of consensus"
misc_feature	8017..8605
	/note="CpG island"
	/evidence=not_experimental
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repeat_region	12659..13001
	/note="LIMB6 repeat: matches 4844..5199 of consensus"
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	/note="LIMB6 repeat: matches 4822..4844 of consensus"
repeat_region	13627..13881
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repeat_region	13883..13938
	/note="28 copies 2 mer tg 96% conserved"
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	/note="LIMB6 repeat: matches 4442..4609 of consensus"
repeat_region	14734..14909
	/note="LIMB6 repeat: matches 4265..4442 of consensus"
repeat_region	14919..14956
	/note="tRNA-Glu-GAG repeat: matches 1..38 of consensus"
repeat_region	14957..14986
	/note="LIMB6 repeat: matches 4243..4276 of consensus"
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	/note="LIPAB repeat: matches 5714..6155 of consensus"
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repeat_region	17572..17808
	/note="MIR16 repeat: matches 3..221 of consensus"
repeat_region	18105..18136
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repeat_region	20000..20164
	/note="AluIo/FRAM repeat: matches 134..302 of consensus"
misc_feature	complement(20889..21207)
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	/note="33 copies 2 mer aa 72% conserved"
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	/note="LIR16C repeat: matches 56..338 of consensus"
misc_feature	25931..26500
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misc_feature	25983..26305
	/note="match: GSS: Em:A0085575"
misc_feature	26038..26355
	/note="match: GSS: Em:A0092382"
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	/note="LIM4 repeat: matches 6164..6300 of consensus"
repeat_region	34383..34547
	/note="FRAM repeat: matches 2..166 of consensus"
repeat_region	35805..35940
	/note="AluSg/x repeat: matches 1..136 of consensus"
repeat_region	36989..37035
	/note="LIM1 repeat: matches 549..569 of consensus"
repeat_region	37476..37780
	/note="AluSg1 repeat: matches 1..304 of consensus"
repeat_region	38469..38658
	/note="AluSg/x repeat: matches 99..288 of consensus"
repeat_region	42358..42471
	/note="MERB1 repeat: matches 3..113 of consensus"
repeat_region	42487..42712
	/note="LIR33 repeat: matches 1..215 of consensus"
repeat_region	43325..43381
	/note="FRAM repeat: matches 1..157 of consensus"
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	/note="match: GSS: Em:A0461520"
	complement(43496..43898)
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	/evidence=not_experimental
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repeat_region	46455..46798
	/note="MER46 repeat: matches 1..236 of consensus"
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	/note="LIMC5 repeat: matches 7535..7849 of consensus"
repeat_region	47116..47171
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repeat_region	47814..47877
	/note="32 copies 2 mer at 78% conserved"
repeat_region	48284..48764
	/note="LIMC5 repeat: matches 6957..7443 of consensus"
gene	49654..100375

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 14:49:43 ; Search time 70178 Seconds
(Without alignments)
11958.699 Million cell updates/sec

Title: US-09-982-091A-5_COPY_30001_58837

Perfect score: 28837

Sequence: 1 atagtatccagcaatttcac.....tatgcagcagttccctgag 28837

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.in.*
18: em.mu.*
19: em.mu.*
20: em.mu.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pin.*
35: em.htg.rtd.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	28837	100.0	194296	9	AL354864	AL354864 Human DNA
2	4624	16.0	111862	2	AL139143	AL139143 Homo sapi
3	1166	4.0	111862	2	AL139143	AL139143 Homo sapi
4	484	1.7	2934	9	AC096303	AC096303 Homo sapi
5	361	1.3	2579	9	BC026909	BC026909 Homo sapi
6	340	1.2	466	6	AX333105	AX333105 Sequence
7	340	1.2	466	11	G30470	G30470 human STS S
8	299	1.0	2394	9	AK096466	AK096466 Homo sapi
9	291	1.0	4756	9	AF297866	AF297866 Homo sapi
10	247	0.9	111744	2	AC099686	AC099686 Homo sapi
11	247	0.9	111744	2	AC023947	AC023947 Homo sapi
12	246	0.9	161613	2	AC092450_4	Continuation (5 of
13	246	0.9	110000	2	AC092450_6	Continuation (7 of
14	245	0.8	80485	9	HSJ231P7P	Continuation (5 of
15	245	0.8	80485	9	HSJ231P7P	Continuation (5 of
16	244	0.8	101077	2	AC024051	AC024051 Homo sapi
17	244	0.8	163782	9	AC011238	AC011238 Homo sapi
18	244	0.8	187110	2	AC084224	AC084224 Homo sapi
19	243	0.8	117303	9	AL773543	AL773543 Human DNA
20	243	0.8	141221	9	AL713888	AL713888 Human DNA
21	243	0.8	170769	9	AC009122	AC009122 Homo sapi
22	243	0.8	202423	2	AC091038	AC091038 Homo sapi
23	242	0.8	79815	9	AC005212	AC005212 Homo sapi
24	242	0.8	118958	9	AC092579	AC092579 Homo sapi
25	242	0.8	176077	2	AC019039	AC019039 Homo sapi
26	242	0.8	185281	2	AC011214	AC011214 Homo sapi
27	242	0.8	189008	2	AP001491	AP001491 Homo sapi
28	242	0.8	207295	9	AL353572	AL353572 Human DNA
29	242	0.8	207818	9	AC019206	AC019206 Homo sapi
30	241	0.8	102479	9	AC115107	AC115107 Homo sapi
31	241	0.8	108048	9	AC115108	AC115108 Homo sapi
32	241	0.8	117051	9	AC115106	AC115106 Homo sapi
33	241	0.8	138993	2	AC087653	AC087653 Homo sapi
34	241	0.8	186428	9	AC016355	AC016355 Homo sapi
35	239	0.8	39441	9	AC005565	AC005565 Homo sapi
36	239	0.8	41073	9	AC005567	AC005567 Homo sapi
37	239	0.8	122783	2	AF238376	AF238376 Homo sapi
38	239	0.8	142839	9	AL356218	AL356218 Human DNA
39	239	0.8	155221	9	AC069335	AC069335 Homo sapi
40	239	0.8	166553	2	AL844523	AL844523 Homo sapi
41	239	0.8	187656	2	AC020564	AC020564 Homo sapi
42	239	0.8	234626	2	AC009095	AC009095 Homo sapi
43	238	0.8	165221	9	AP000457	AP000457 Homo sapi
44	238	0.8	176851	2	AC016372	AC016372 Homo sapi
45	238	0.8	290766	2	AL583862	AL583862 Homo sapi

ALIGNMENTS

RESULT 1
AL354864
LOCUS
DEFINITION

194296 bp DNA linear PRI 04-APR-2001
Human DNA sequence from clone RP11-435D7 on chromosome 1. Contains
ESTs, STSS, GSSs and Cpg Islands. Contains a novel gene and the 5'
part of the PSMB2 gene for Proteasome (prosome, macropain) subunit
2, beta type, complete sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL354864
AL354864.16 GI:10185566
HTG; Cpg island; macropain; prosome; proteasome; PSMB2.
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194296)

Pred. No. is the number of results predicted by chance to have a

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Db      91697  CCACCACCGCCGGCTAAATTTTGTATTTTAGTAGACGGGGTTTCACCATGTTAGCC 91756
OY      27674  AGGATGGTCTTCTGATCTCTGACCTCGTGATCCGCCCGCTCGGCTCC 27722
Db      91757  AGGATGGTCTTCTGATCTCTGACCTCGTGATCCGCCCGCTCGGCTCC 91805

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RESULT 15

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AP000729
LOCUS      Homo sapiens genomic DNA, chromosome 11 clone:RP11-699D4, complete
DEFINITION
ACCESSION  AP000729
VERSION    AP000729.4 GI:22415810
KEYWORDS   HTG.
SOURCE     Homo sapiens DNA, clone:RP11-699D4.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

JOURNAL Homo sapiens genomic DNA

REFERENCE Published Only in Database (1999)

AUTHORS 2 (bases 1 to 160535)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

JOURNAL Direct Submission

TITLE Submitted (16-NOV-1999) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT On Aug 21, 2002 this sequence version replaced gi:11071942.

FEATURES

SOURCE Location/Qualifiers

1..160535

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/db_xref="taxon:9606"

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/map="11q"

/clone="RP11-699D4"

BASE COUNT 39840 a 39815 c 41519 g 39361 t

ORIGIN

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Best Local Similarity 100.0%; Pred No. 1.5e-44;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      75532  CCACCACCGCCGGCTAAATTTTGTATTTTAGTAGACGGGGTTTCACCATGTTAGCC 75591
OY      27674  AGGATGGTCTTCTGATCTCTGACCTCGTGATCCGCCCGCTCGGCTCC 27722
Db      75592  AGGATGGTCTTCTGATCTCTGACCTCGTGATCCGCCCGCTCGGCTCC 75640

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Search completed: June 24, 2003, 10:33:52
Job time : 58874 secs

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60057 63347 contig of 1291 bp in length
63448 66289 contig of 2842 bp in length
66390 69592 contig of 3203 bp in length
69693 72010 contig of 2318 bp in length
72111 75133 contig of 3023 bp in length
75234 77770 contig of 2537 bp in length
77871 81172 contig of 3302 bp in length
81273 83633 contig of 2583 bp in length
83734 86173 contig of 3318 bp in length
86417 89734 contig of 3469 bp in length
89835 93403 contig of 2587 bp in length
93404 95990 contig of 2403 bp in length
96091 98493 contig of 2736 bp in length
98594 101329 contig of 100 bp in length
101430 102985 contig of 1556 bp in length
103086 104913 contig of 1828 bp in length
105014 107643 contig of 2630 bp in length
107744 109302 contig of 1559 bp in length
109403 111110 contig of 1708 bp in length
111211 112850 contig of 1640 bp in length
112951 114294 contig of 1344 bp in length
114395 11578 contig of 1184 bp in length
115679 117097 contig of 1419 bp in length
117198 118741 contig of 1544 bp in length
118842 120316 contig of 1475 bp in length
120417 121928 contig of 1512 bp in length
122029 123611 contig of 1583 bp in length
123712 125176 contig of 1465 bp in length
125277 126313 contig of 1037 bp in length
126414 126497 contig of 84 bp in length
126598 127661 contig of 1064 bp in length

```

Sequence updated (26-May-2000).

NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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12428 12428: contig of 12428 bp in length
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20729 29692: contig of 8964 bp in length
29693 29792: gap of 100 bp
29793 38212: contig of 8420 bp in length
38213 38312: gap of 100 bp
38313 45303: contig of 6991 bp in length
45304 45403: gap of 100 bp
45404 49522: contig of 4119 bp in length
49523 49622: gap of 100 bp
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52790 52889: gap of 100 bp
52890 56364: contig of 3475 bp in length
56365 56464: gap of 100 bp
56465 59956: contig of 3492 bp in length
59957 60056: gap of 100 bp
60057 63347: contig of 3291 bp in length
63348 63447: gap of 100 bp
63448 66289: contig of 2842 bp in length
66290 66389: gap of 100 bp
66390 69592: contig of 3203 bp in length
69593 69692: gap of 100 bp
69693 72010: contig of 2318 bp in length
72011 72110: gap of 100 bp
72111 75133: contig of 3023 bp in length
75134 75233: gap of 100 bp
75234 77770: contig of 2537 bp in length
77771 77870: gap of 100 bp
77871 81172: contig of 3302 bp in length
81173 81272: gap of 100 bp
81273 83633: contig of 2583 bp in length

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83634 83733: gap of 100 bp
83734 86173: contig of 2583 bp in length
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95991 96090: gap of 100 bp
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111111 111210: gap of 100 bp
111211 112850: contig of 1640 bp in length
112851 112950: gap of 100 bp
112951 114294: contig of 1344 bp in length
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120317 120416: gap of 100 bp
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122029 123611: contig of 1583 bp in length
123612 123711: gap of 100 bp
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125177 125276: gap of 100 bp
125277 126313: contig of 1037 bp in length
126314 126413: gap of 100 bp
126414 126497: contig of 84 bp in length
126498 126597: gap of 100 bp
126598 127661: contig of 1064 bp in length.

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FEATURES

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Query Match

Best Local Similarity 0.4%; Score 109; DB 2; Length 127661; Pred. No. 1,5e-44; Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27614 CCACCACCCCGCGCTATTGTTGATTGTTAGTAGACACGCGTTCCACCATGTAGCC 27673

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complement(13406..13428)
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complement(13429..13690)
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complement(13691..13871)
repeat_region /rpt_family="Zaphod"
complement(13882..14103)
repeat_region /rpt_family="L1MED"
14104..14309
repeat_region /rpt_family="(TA)n"
complement(14310..14329)
repeat_region /rpt_family="L1MED"
complement(14330..14634)
repeat_region /rpt_family="AluY"
complement(14635..14760)
repeat_region /rpt_family="L1MED"
14763..15000
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15047..15460
repeat_region /rpt_family="MSTA"
15468..15692
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complement(15693..15993)
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15994..16107
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17142..17458
repeat_region /rpt_family="MLTIG3"
complement(17567..18296)
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complement(18309..18781)
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18792..18813
repeat_region /rpt_family="(TA)n"
complement(18817..19100)
repeat_region /rpt_family="AluSg"
complement(19114..19305)
repeat_region /rpt_family="L1MB2"
complement(19306..19582)
repeat_region /rpt_family="AluSx"
complement(19583..21037)
repeat_region /rpt_family="L1MB2"
complement(21038..21438)
repeat_region /rpt_family="MSTA"
complement(21439..21616)
repeat_region /rpt_family="L1MB2"
21617..22779
repeat_region /rpt_family="L1PA16"
complement(22929..23054)
repeat_region /rpt_family="L1MB2"
complement(23047..23448)
repeat_region /rpt_family="L1MD1"
complement(23527..23840)
repeat_region /rpt_family="AluJo"
complement(23842..24062)
repeat_region /rpt_family="L1MD1"
complement(24063..24332)
repeat_region /rpt_family="AluJo"
complement(24333..24436)
repeat_region /rpt_family="L1MD1"
24437..24483
repeat_region /rpt_family="MADE1"
complement(24484..25973)
Query Match 0.43; Score 112; DB 9; Length 221475;
Best Local Similarity 100.0%; Pred. No. 4.3e-46;

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Matches 112: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29776 CAGCCTGACCAACATGGTGAACCCCGTCTCTACTAAATACAAAAATAGCTGGCATG 29835
 |||||
 Db 191326 CAGCCTGACCAACATGGTGAACCCCGTCTCTACTAAATACAAAAATAGCTGGCATG 191385
 |||||

OY 29836 GTGGCGCATGCGCTGTAATCCAGCTACTTGGGAGGCTGAGCGAGGAATG 29887
 |||||
 Db 191386 GTGGCGCATGCGCTGTAATCCAGCTACTTGGGAGGCTGAGCGAGGAATG 191437
 |||||

RESULT 14
 AP001261

LOCUS AP001261 127661 bp DNA linear HTG 31-MAY-2000
 DEFINITION Homo sapiens chromosome 11 clone RP11-655A22 map 11q13, WORKING
 DRAFT SEQUENCE, 40 unordered pieces.
 ACCESSION AP001261
 VERSION AP001261.2 GI:8131598
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens DNA, clone:RP11-655A22.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens 127,661 genomic DNA of 11q13
 2 (bases 1 to 127661)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
 Japan (E-mail:hattori@gscc.riken.go.jp,
 URL:http://hgsc.gsc.riken.go.jp/, Tel:81-42-778-9923,
 Fax:81-42-778-9924)
 On May 31, 2000 this sequence version replaced gi:7106129.

COMMENT
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center (GSC)
 Center code: RIKEN
 Web site: http://hgsc.gsc.riken.go.jp/
 Contact: hattori@gscc.riken.go.jp
 ----- Project Information
 Center project name: HumDraft1
 Center clone name: RP11-655A22
 ----- Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.950329
 Consensus quality: 105777 bases at least Q40
 Consensus quality: 115033 bases at least Q30
 Consensus quality: 120045 bases at least Q20
 Insert size: 123761; sum-of-contigs
 Quality coverage: 4.16x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
 40 contigs. The true order of the pieces is not known and the
 order in this sequence record is arbitrary. Gaps between the
 contigs are represented as runs N, but the exact sizes of the gaps
 are unknown. This record will be updated with the finished sequence
 as soon as it is available and the accession number will be
 preserved

1	12428	contig of	12428	bp in length
12529	20628	contig of	8100	bp in length
20729	29692	contig of	8964	bp in length
29793	38212	contig of	8420	bp in length
38313	45303	contig of	6991	bp in length
45404	49522	contig of	6991	bp in length
49623	52789	contig of	3167	bp in length
52890	56364	contig of	3475	bp in length
56465	59956	contig of	3492	bp in length

Query Match 0.48; Score 113; DB 2; Length 174562;
 Best Local Similarity 100.0%; Pred. No. 1.3e-46;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27610 CCCACACACACGCGCCGCTAATTTTGTATTTTGTAGACAGCGGCTTCACATGTT 27669
 130371 CCCACACACACGCGCCGCTAATTTTGTATTTTGTAGACAGCGGCTTCACATGTT 130312

QY 27670 AGCCAGATGCTCTGATCTCTGATCGCTGATCGCGCCGCTCCGCTCC 27722
 130311 AGCCAGATGCTCTGATCTCTGATCGCTGATCGCGCCGCTCCGCTCC 130259

RESULT 13
 AC009562 221475 bp DNA linear PRI 12-JAN-2002
 LOCUS Homo sapiens chromosome 15, clone RP11-348B17, complete sequence.
 DEFINITION AC009562
 AC009562
 VERSION AC009562.9 GI:18034741
 KEYWORDS HGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.

REFERENCE
 AUTHORS Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
 TITLE Birren B., Linton L., Nusbaum C. and Lander E.
 JOURNAL Homo sapiens chromosome 15, clone RP11-348B17
 REFERENCE
 AUTHORS 2 (bases 1 to 221475)
 Birren B., Linton L., Nusbaum C., Lander E., Allen N., Anderson M.,
 Baker J., Baldwin J., Barna N., Beckert R., Bern J., Brown A.,
 Castle A., Cerny J., Colangelo M., Collins S., Collumore A.,
 Cooke P., DeRellano K., Depayre E., Devon K., Dewar K.,
 Donelan L., Doyle M., Ferreira P., FitzHugh W., Forrest C.,
 Funke R., Gage D., Galagan J., Gardyna S., Gilbert D., Grant G.,
 Hagos B., Heaford A., Horton L., Howland J. C., Jones C., Kann L.,
 Karatas A., Lehoczy J., Lieu C., Locke K., Macdonald P.,
 Marquis N., McEwan P., McGurk A., McKernan K., McLaughlin J.,
 Meldrum J., Molla M., Morris W., Morrow J., Mychaleckyj J.,
 Naylor J., Niloff M., O'Connor T., O'Donnell P., Pavlin B.,
 Peterson K., Pollara V., Riley R., Roberts D., Roy A., Severy P.,
 Stange-Thomann N., Stojanovic N., Stone C., Subramanian A.,
 Testa J., Toriella-Miller I., Vassiliev H., Vo A., Wagner A.,
 Wheeler J., Wu X., Wyman D., Ye W. J. and Zody M.

TITLE
 JOURNAL Submitted (27-AUG-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE
 AUTHORS 3 (bases 1 to 221475)
 Birren B., Linton L., Nusbaum C., Lander E., Allen N., Anderson M.,
 Anderson S., Barna N., Bastien V., Boguslavsky L., Boukhgalter B.,
 Brown A., Camarata J., Campiano A., Chang J., Chazaro B.,
 Choquet Y., Colangelo M., Collins S., Collumore A., Cooke P.,
 Cooke P., DeRellano K., Dewar K., Diaz J. S., Dodge S., Faro S.,
 Ferreira P., FitzHugh W., Gage D., Galagan J., Gardyna S.,
 Glade S., Gord S., Goyette M., Graham L., Grand-Pierre N.,
 Hagos B., Heaford A., Horton L., Hulme M., Iliev I., Johnson R.,
 Jones C., Kann A., Karatas A., Kells C., Laroque K.,
 Lamazares R., Landers T., Lehoczy J., Levine R., Liu G.,
 Maclean C., Macdonald P., Major J., Marquis N., Matthews C.,
 McCarthy M., McEwan P., McKernan K., McNeesters R., Meldrum J.,
 Meneus L., Milnova T., Mlenka V., Murphy T., Naylor J., Nguyen C.,
 Oliver J., Peterson K., Phunkhang P., Pierre N., O'Neill D.,
 Raymond C., Retta R., Rieback M., Riley R., Rise C., Rogov P.,
 Roman J., Roselli M., Roy A., Santos R., Schauer S., Schnupack R.,
 Seaman S., Severy P., Spencer B., Stange-Thomann N., Stojanovic N.,
 Straus N., Subramanian A., Talamas J., Testa J., Theodore J.,
 Topham K., Travers M., Travis N., Triggillo J., Vassiliev H.,
 Viell R., Vo A., Wilson B., Wu X., Wyman D., Ye W. J., Young C.,
 Zainoun J., Zembek L., Zimmer A. and Zody M.

TITLE
 JOURNAL Direct Submission
 Submitted (12-JAN-2002) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 2, 2002 this sequence version replaced g1:15706125.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: 11689

Center clone name: 348_B_17

FEATURES

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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="15"
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 /complement(50..555)
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 /rpt_family="L2"
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 /complement(9897..9949)
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 /rpt_family="AluSx"
 /complement(10613..11039)
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Db        403 CAAAACGTGT 411

RESULT 10
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LOCUS    AX069706          386 bp      DNA      linear      PAT 25-JAN-2001
DEFINITION Sequence 178 from Patent WO0102568.
ACCESSION AX069706
VERSION   AX069706.1 GI:12579451
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
TITLE    Human genes and gene expression products
JOURNAL  Patent: WO 0102568-A 178 11-JAN-2001;
CHIRON CORPORATION (US) : HYSEQ, INC. (US)
FEATURES
source    1..386
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            /db_xref="taxon:9606"
misc_feature 1..386
            /note="n = A,T,C or G"
BASE COUNT 128 a 76 c 116 g 65 t 1 others
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Query Match      0.4%; Score 135; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10087 AGATTCCAGATGAAGACATATTTCTAGTAGAAGTTGAAAACAGGAGGTTCTACAAGA 10146
Db      251 AGATTCCAGATGAAGACATATTTCTAGTAGAAGTTGAAAACAGGAGGTTCTACAAGA 310

QY      10147 CAGTGATTCGAAACAGAGGACACAAATGCCTCTCCAGAGAAAACACTATGACAGTGC 10206
Db      311 CAGTGATTCGAAACAGAGGACACAAATGCCTCTCCAGAGAAAACACTATGACAGTGC 370

QY      10207 CGAGGAGGAAAATAA 10221
Db      371 CGAGGAGGAAAATAA 385

RESULT 11
AX071923
LOCUS    AX071923          406 bp      DNA      linear      PAT 25-JAN-2001
DEFINITION Sequence 2395 from Patent WO0102568.
ACCESSION AX071923
VERSION   AX071923.1 GI:12582274
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
TITLE    Human genes and gene expression products
JOURNAL  Patent: WO 0102568-A 2395 11-JAN-2001;
CHIRON CORPORATION (US) : HYSEQ, INC. (US)
FEATURES
source    1..406
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="11"
            /clone="CIT987SK-1012F4"
BASE COUNT 21150 a 29998 c 29519 g 21315 t 72580 others
ORIGIN

BASE COUNT 142 a 73 c 115 g 76 t
ORIGIN

Query Match      0.4%; Score 133; DB 6; Length 406;
Best Local Similarity 99.5%; Pred. No. 5.3e-57;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10087 AGATTCCAGATGAAGACATATTTCTAGTAGAAGTTGAAAACAGGAGGTTCTACAAGA 10146
Db      223 AGATTCCAGATGAAGACATATTTCTAGTAGAAGTTGAAAACAGGAGGTTCTACAAGA 282

QY      10147 CAGTGATTCGAAACAGAGGACACAAATGCCTCTCCAGAGAAAACACTATGACAGTGC 10206
Db      283 CAGTGATTCGAAACAGAGGACACAAATGCCTCTCCAGAGAAAACACTATGACAGTGC 342

QY      10207 CGAGGAGGAAAATAAAGAGAAATTTATATGCTGGGAAAAATACAAAAATCAAAAGGATTTA 10266
Db      343 CGAGGAGGAAAATAAAGAGAAATTTATATGCTGGGAAAAATACAAAAATCAAAAGGATTTA 402

QY      10267 CAAA 10270
Db      403 CAAA 406

RESULT 12
AC005848/c
LOCUS    AC005848          174562 bp      DNA      linear      HTG 30-AUG-2001
DEFINITION Homo sapiens chromosome 11 clone CIT987SK-1012F4, 6 unordered
            pieces.
ACCESSION AC005848
VERSION   AC005848.1 GI:3779014
KEYWORDS  HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Smith,D.R.
TITLE    Sequencing of Human Chromosome 10
JOURNAL  Unpublished
REFERENCE
AUTHORS  Smith,D.R.
TITLE    Direct Submission
JOURNAL  Submitted (22-OCT-1998) Genome Therapeutics Corporation, 100 Beaver
            Street, Waltham, MA 02154, USA
COMMENT   * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence.
            * as soon as it is available and the accession number will
            * be preserved.
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            * 1 4561: contig of 4561 bp in length
            * 4562 19077: gap of unknown length
            * 19078 30350: contig of 11273 bp in length
            * 30351 44866: gap of unknown length
            * 44867 58909: contig of 14043 bp in length
            * 58910 73424: gap of unknown length
            * 73425 90412: contig of 16988 bp in length
            * 90413 104927: gap of unknown length
            * 104928 130554: contig of 25627 bp in length
            * 130555 145069: gap of unknown length
            * 145070 174562: contig of 29493 bp in length.
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            * Location/Qualifiers
            * 1..174562
            * /organism="Homo sapiens"
            * /db_xref="taxon:9606"
            * /chromosome="11"
            * /clone="CIT987SK-1012F4"
BASE COUNT 21150 a 29998 c 29519 g 21315 t 72580 others
ORIGIN

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OY 10147 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 10206
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DB 286 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 345
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OY 10207 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATACAAAATCAAAAGATTTA 10266
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DB 346 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATACAAAATCAAAAGATTTA 405
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OY 10267 CAAACTGTGGCGAGCA 10283
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DB 406 CAAACTGTGGCGAGCA 422

RESULT 7
AX245923 393 bp DNA linear PAT 28-SEP-2001
LOCUS Sequence 853 from Patent W00166753.
ACCESSION AX245923
VERSION AX245923.1 GI:15860597
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 393)
REFERENCE
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Civenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Cralin,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 853 13-SEP-2001;
Chiron Corporation (US) ; Hyseq Inc. (US)
FEATURES
source 1..393
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 135 a 74 c 109 g 74 t 1 others
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Best Local Similarity 100.0%; Pred. No. 8.9e-78;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 221 AGATTCAGATGAAGACATATTTTGAAGTAAGAAAGTTCACAGCA 280
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OY 10147 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 10206
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DB 281 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 340
    |||||||
OY 10207 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATCAAAATCAAA 10259
    |||||||
DB 341 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATCAAAATCAAA 393
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RESULT 8
AX245847 408 bp DNA linear PAT 28-SEP-2001
LOCUS Sequence 777 from Patent W00166753.
ACCESSION AX245847
VERSION AX245847.1 GI:15860521.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 408)
REFERENCE
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Civenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Cralin,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 777 13-SEP-2001;
Chiron Corporation (US) ; Hyseq Inc. (US)
FEATURES
source 1..408
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 134 a 78 c 119 g 76 t 1 others
ORIGIN

Query Match 0.5%; Score 164; DB 6; Length 408;
Best Local Similarity 100.0%; Pred. No. 4.2e-73;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10087 AGATTCAGATGAAGACATATTTTGAAGTAAGAAAGTTCACAGCA 10146
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DB 244 AGATTCAGATGAAGACATATTTTGAAGTAAGAAAGTTCACAGCA 303
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OY 10147 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 10206
    |||||||
DB 304 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 363
    |||||||
OY 10207 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATCAAA 10250
    |||||||
DB 364 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATCAAA 407
    |||||||

RESULT 9
AX071922 411 bp DNA linear PAT 25-JAN-2001
LOCUS Sequence 2394 from Patent W00102568.
ACCESSION AX071922
VERSION AX071922.1 GI:12582273
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 411)
REFERENCE
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Civenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Stache-Cralin,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0102568-A 2394 11-JAN-2001;
CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
FEATURES
source 1..411
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 143 a 74 c 116 g 78 t
ORIGIN

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DB 283 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTTCATGACAGTGC 342
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OY 10207 CGAGGAGGAAATTAAGAGAAATTTATATGCTGGGAAAAATCAAAAGATTTA 10266
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BASE COUNT 57648 a 40434 c 38526 g 55039 t 2043 others
ORIGIN

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Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 20078 ATATCACTGACTGGATTGTCTATTTATTTTCCCTCTCTGAAAAAATTTGACTTTGCTAT 20137
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DB 2896 ATTTAGTAAGTGGCCAAATTAATCAAAATAGGGAATTTGATCCAGCACTTTG 2837
QY 20198 GGAGGCCAAGTGGCTGATCATTTGAGTTCAGGAGTTCGAGACCAAGCTGGCTAACATG 20257
DB 2836 GGAGGCCAAGTGGCTGATCATTTGAGTTCAGGAGTTCGAGACCAAGCTGGCTAACATG 2777
QY 20258 GTGAAACCCCTGCTCTACTAAAAATACAAAAAATAGCTGGCATGGTGGCTCACT 20317
DB 2776 GTGAAACCCCTGCTCTACTAAAAATACAAAAAATAGCTGGCATGGTGGCTCACT 2717
QY 20318 GTAACCTCAGCTACTCAGGAGTTCAGGAGGAGATCGCTTGAACCCCTGGAGATGGAGG 20377
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DB 2596 CTCANAA 2590

RESULT 5
AX246208
LOCUS AX246208
DEFINITION Sequence 1138 from Patent WO0166753.
ACCESSION AX246208
VERSION AX246208.1 GI:15860882

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 421)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 1138 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
FEATURES Location/Qualifiers
source 1..421
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 153 a 72 c 111 g 85 t
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Best Local Similarity 100.0%; Pred. No. 6.7e-108;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
AX246209
LOCUS AX246209
DEFINITION Sequence 1139 from Patent WO0166753.
ACCESSION AX246209
VERSION AX246209.1 GI:15860883
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 422)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 1139 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
FEATURES Location/Qualifiers
source 1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 146 a 78 c 119 g 79 t
ORIGIN
Query Match 0.7%; Score 197; DB 6; Length 422;
Best Local Similarity 100.0%; Pred. No. 3e-90;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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DEFINITION Homo sapiens chromosome 1 clone RP11-552D8, WORKING DRAFT SEQUENCE.
ACCESSION AC118559 AL445488
VERSION AC118559.1 GI:20177709
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILL; HTGS_ACTIVEFIN.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 193690)
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Apr 18, 2002 this sequence version replaced g1:10803120.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Drafting Center: SC
----- Project Information
Center project name: chr-1
Center clone name: RP11-552D8 (sc0738)
----- Summary Statistics

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Sequencing vector: plasmid; 3% of reads
Sequencing vector: plasmid; 108752; 6% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179778 bases at least Q40
Consensus quality: 186231 bases at least Q40
Consensus quality: 189706 bases at least Q20
Insert size: 192090; sum-of-contigs
Quality coverage: 5.1x in Q20 bases; sum-of-contigs
Note: Full shotgun coverage (8x) has been generated for a subclone
of the original BAC, comprising only the unique sequence between
its two neighboring clones in the tiling path, plus enough overlap
to link it to these sequences.
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
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3077 3176: gap of unknown length
3177 6670: contig of 3494 bp in length
6671 6770: gap of unknown length
6771 10542: contig of 3772 bp in length
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15197 15297: gap of unknown length
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69465 82334: contig of 12870 bp in length
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RESULT 3
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LOCUS Homo sapiens Hu-Claspin mRNA, complete cds.
DEFINITION AF297866
ACCESSION AF297866
VERSION AF297866.1 GI:10944333
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4756)
AUTHORS Kumagai, A. and Dunphy, W.G.
TITLE Claspin, a novel protein required for the activation of Chk1 during
a DNA replication checkpoint response in Xenopus egg extracts
JOURNAL Mol. Cell 6 (4), 839-849 (2000)
MEDLINE 21000493
PUBMED 11090622
REFERENCE 2 (bases 1 to 4756)
AUTHORS Kumagai, A. and Dunphy, W.G.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-2000) Biology, California Institute of
Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA
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FEATURES

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CDS

1626 a 896 c 1227 g 1007 t

BASE COUNT

1626 a 896 c 1227 g 1007 t

ORIGIN

Query Match

1.9%; Score 575; DB 9; Length 4756;

Best Local Similarity

100.0%; Pred. No. 1.4e-286;

Matches 575; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

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OY 14900 CGAGACTCCACCATTCAGCTCCAGCTGGGAGAGAGCAGAGCTCTTCAAAAAA 14959
Db 55057 CGAGACTCCACCATTCAGCTCCAGCTGGGAGAGAGCAGAGCTCTTCAAAAAA 55116
OY 14960 AAAAAAAAAAAGCTTGTGATA - GTTAATATAAAAAGAGTACATTCTACTGTGT 15018
Db 55117 AAAAAAAAAAAGCTTGTGATA - GTTAATATAAAAAGAGTACATTCTACTGTGT 55176
OY 15019 TATGTATTTAGGAATTAATATTTCCCTTCCATCTCAATTAATTAATTTTCTGTA 15078
Db 55177 TATGTATTTAGGAATTAATATTTCCCTTCCATCTCAATTAATTAATTTTCTGTA 55236
OY 15079 ATCTGAGTCAATCTTAAGACATTAAGAAACATCAATTAATTTTACTGCTAAGA 15138
Db 55237 ATCTGAGTCAATCTTAAGACATTAAGAAACATCAATTAATTTTACTGCTAAGA 55296
OY 15139 GAACATTTTGGTCACTTAATTAATCTGTAACCCAGATTTCTTTGTTTCACTCAT 15198
Db 55297 GAACATTTTGGTCACTTAATTAATCTGTAACCCAGATTTCTTTGTTTCACTCAT 55356
OY 15199 CAACAAATTAATTAAGTATCTAATAGTAAAGTTGGGGCATACCAAGATTAATCT 15258
Db 55357 CAACAAATTAATTAAGTATCTAATAGTAAAGTTGGGGCATACCAAGATTAATCT 55416
OY 15259 GACATTTAAGTATCTAATAGTAAAGTTGGGGCATACCAAGATTAATCT 15318
Db 55417 GACATTTAAGTATCTAATAGTAAAGTTGGGGCATACCAAGATTAATCT 55476
OY 15319 TAAAGATTAAGGAGAGAAAAATGTAATGATCTTGTATTAATGATATGTCATTGTA 15378
Db 55477 TAAAGATTAAGGAGAGAAAAATGTAATGATCTTGTATTAATGATATGTCATTGTA 55536
OY 15379 ATTGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15438
Db 55537 ATTGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 55596
OY 15439 AAAGTACTGGGAAATTCAGAGAAATTAATTTCTTCAATGAATAGTTAAAGACAGC 15498
Db 55597 AAAGTACTGGGAAATTCAGAGAAATTAATTTCTTCAATGAATAGTTAAAGACAGC 55656
OY 15499 CTGAAGATTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15558
Db 55657 CTGAAGATTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 55716
OY 15559 TCTTCTGCTTGTCCCTACCTATACCTTACCTGCTCCTCAGTGCAGACATTTGAG 15618
Db 55717 TCTTCTGCTTGTCCCTACCTATACCTTACCTGCTCCTCAGTGCAGACATTTGAG 55776
OY 15619 CACTTGTATTTATCAATTAATGAATGATCCCTCAACACTGATCAAGTATTTACCAAT 15678
Db 55777 CACTTGTATTTATCAATTAATGAATGATCCCTCAACACTGATCAAGTATTTACCAAT 55836
OY 15679 TGAATTAATTTCCGACCTTATAGATAGAGTGGATGCTCCCACTGCTTGGAGCACT 15738
Db 55837 TGAATTAATTTCCGACCTTATAGATAGAGTGGATGCTCCCACTGCTTGGAGCACT 55896
OY 15739 ATGAATGCTGTTAAGAGTAAAGCTTTGAGAAACAGAGATTTGAATCTGAACAG 15798
Db 55897 ATGAATGCTGTTAAGAGTAAAGCTTTGAGAAACAGAGATTTGAATCTGAACAG 55956
OY 15799 CATAGTAAATTTTAACTGATTAAGGCAATTAAGCTTTCAGAGATCTTTTCTTAA 15858
Db 55957 CATAGTAAATTTTAACTGATTAAGGCAATTAAGCTTTCAGAGATCTTTTCTTAA 56016
OY 15859 AAAGAGAAAGGACAGACAGTGTGACACAGTGTAGTTCCAGCTACCTCGGAGGCTG 15918
Db 56017 AAAGAGAAAGGACAGACAGTGTGACACAGTGTAGTTCCAGCTACCTCGGAGGCTG 56076

QY	10461	CAAAAAGAACCTTGTAGAAAGAGAGAAAAATGAAAAAATATAGACAGCTAAAAAGA	10520
Db	50623	CAAAAAGAACCTTGTAGAAAGAGAGAAAAATGAAAAAATATAGACAGCTAAAAAGA	50682
QY	10521	AGAAACAAAAAACCGAGTACATTTTAAAGAAATAATGCTATGCTGGGTAGGTTAC	10580
Db	50683	AGAAACAAAAAACCGAGTACATTTTAAAGAAATAATGCTATGCTGGGTAGGTTAC	50742
QY	10581	ATTTTAGAAAAAGTGTCTGTATTAGACTTGGAGTGTCTTCGCTCTCGACTATTCGTTG	10640
Db	50743	ATTTTAGAAAAAGTGTCTGTATTAGACTTGGAGTGTCTTCGCTCTCGACTATTCGTTG	50802
QY	10641	AATTACTATTTTGGTGGAGAATTATTCACATAGGTATGTATTTAAACTACTGCT	10700
Db	50803	AATTACTATTTTGGTGGAGAATTATTCACATAGGTATGTATTTAAACTACTGCT	50862
QY	10701	CTTGCCACGAGTGACAGTGTGTGATACGTCTATATCCACAGCACTTGGAGAGCTGAGGCCAGA	10760
Db	50863	CTTGCCACGAGTGACAGTGTGTGATACGTCTATATCCACAGCACTTGGAGAGCTGAGGCCAGA	50922
QY	10761	GGGTACTTAAGCCACAGAGAGTTCAGAAACAGCCTTAGCAACAGATGATCCCATCTCT	10820
Db	50923	GGGTACTTAAGCCACAGAGAGTTCAGAAACAGCCTTAGCAACAGATGATCCCATCTCT	50982
QY	10821	ACAAAAAATTTAAAAATTTAGTGGGTGTGGTGGCCGATAGCCAGCTGATAGTCCCACTA	10880
Db	50983	ACAAAAAATTTAAAAATTTAGTGGGTGTGGTGGCCGATAGCCAGCTGATAGTCCCACTA	51042
QY	10881	CTTGGGAGGCTGACAGTGGGAGAAATCACTTGAGCCCAAGGAAGTGCAGCGCTGCATAGACT	10940
Db	51043	CTTGGGAGGCTGACAGTGGGAGAAATCACTTGAGCCCAAGGAAGTGCAGCGCTGCATAGACT	51102
QY	10941	CTAATTGTACACATGCATTCCTCAGCTGGATGACAGATGAGACCCGTCTCAAAAAAAA	11000
Db	51103	CTAATTGTACACATGCATTCCTCAGCTGGATGACAGATGAGACCCGTCTCAAAAAAAA	51162
QY	11001	AAAAACAAAAACCAAAAAACAAACTATGTGCTTATTTATTTGGGTATGCAGAG	11060
Db	51163	AAAAACAAAAACCAAAAAACAAACTATGTGCTTATTTATTTGGGTATGCAGAG	51222
QY	11061	ACATTTCCAAATAAATGGGTTCGTGATTTTCTTATAGACACATAGGAATATCTTGTCT	11120
Db	51223	ACATTTCCAAATAAATGGGTTCGTGATTTTCTTATAGACACATAGGAATATCTTGTCT	51282
QY	11121	GTCCTCAGCTGATGAAAAATTAAGTCAAAAGAGCCTTTTATGATCATACAGTACGTA	11180
Db	51283	GTCCTCAGCTGATGAAAAATTAAGTCAAAAGAGCCTTTTATGATCATACAGTACGTA	51342
QY	11181	GTCCTGTTTCTAAGTCAAGAAAAACATCCGCAATTTAATAACTAGTGGCTTAACAGTA	11240
Db	51343	GTCCTGTTTCTAAGTCAAGAAAAACATCCGCAATTTAATAACTAGTGGCTTAACAGTA	51402
QY	11241	TTTTACTTCAAAAAAATATTACTGTGTTTATTAAGTTAGTTTATGACAGTGCATAAATC	11300
Db	51403	TTTTACTTCAAAAAAATATTACTGTGTTTATTAAGTTAGTTTATGACAGTGCATAAATC	51462
QY	11301	ACAACCTGAGACTCAAAAGATACATGCTGATGAGAAACAGTACAGATGCTTCGATTTT	11360
Db	51463	ACAACCTGAGACTCAAAAGATACATGCTGATGAGAAACAGTACAGATGCTTCGATTTT	51522
QY	11361	ATATGCTTGTCTGTGTATGATGAACATGGGCTTTTCTGGCGCTGATCAAAATGGCATATGA	11420
Db	51523	ATATGCTTGTCTGTGTATGATGAACATGGGCTTTTCTGGCGCTGATCAAAATGGCATATGA	51582
QY	11421	TGTTGTGAATTAATGCAATTTTAAATGATGATTAATGCTTTTGTATTATTAATTA	11480
Db	51583	TGTTGTGAATTAATGCAATTTTAAATGATGATTAATGCTTTTGTATTATTAATTA	51642
QY	11481	GGAAGATGATGTGGAACACAGCAATTAATATACAGTGGCTGTCTGTGTGGATTAAGAGCT	11540
Db	51643	GGAAGATGATGTGGAACACAGCAATTAATATACAGTGGCTGTCTGTGTGGATTAAGAGCT	51702

QY 7165 TACACACATAGTCTGAAGGTAAATTTATACAGCATTTTAAATAATTTTCGTGCATGAAGC 7224
DB TACACACATAGTCTGAAGGTAAATTTATACAGCATTTTAAATAATTTTCGTGCATGAAGC 47383
QY 7225 AAAGCTTTTACTGCGAGCTCATCATATGAGGTGAGGTGGAATTTTTCATCTAGTGGCATC 7284
DB AAAGCTTTTACTGCGAGCTCATCATATGAGGTGAGGTGGAATTTTTCATCTAGTGGCATC 47443
QY 7285 ATGTCAGTGTCAATATTTTGGAAATTTGGAGCAATTTTCAGATTTTCAGGTTAGAGATGTT 7344
DB ATGTCAGTGTCAATATTTTGGAAATTTGGAGCAATTTTCAGATTTTCAGGTTAGAGATGTT 47503
QY 7345 CAACCTGTATTTTCAAGTCATGCGCAATCTGTTTATTCATACAGACTACCCATTTTTC 7404
DB CAACCTGTATTTTCAAGTCATGCGCAATCTGTTTATTCATACAGACTACCCATTTTTC 47563
QY 7405 TCTCACAGGATTTATTTGGAATTTGGAGCAATTTTCAGATTTTCAGGTTAGAGATGTT 7464
DB TCTCACAGGATTTATTTGGAATTTGGAGCAATTTTCAGATTTTCAGGTTAGAGATGTT 47623
QY 7465 TAGTGTGCATATCTAACAAACAGAGCTTTTCCAAAATATAGATACATATTTATACCA 7524
DB TAGTGTGCATATCTAACAAACAGAGCTTTTCCAAAATATAGATACATATTTATACCA 47683
QY 7525 CACCTAAGAGTATCTAGTCAGTGTTCAGATTTTCTTTGACTCAGAGATATTTCAATTTAT 7584
DB CACCTAAGAGTATCTAGTCAGTGTTCAGATTTTCTTTGACTCAGAGATATTTCAATTTAT 47743
QY 7585 TTTATATGCCACTTTAGCATATTTATTTACATTTTACATTTTGTAGTTTGTGAAATCATCTCCGAG 7644
DB TTTATATGCCACTTTAGCATATTTATTTACATTTTGTAGTTTGTGAAATCATCTCCGAG 47803
QY 7645 TTGCAATTTTGTATTTAT 7704
DB TTGCAATTTTGTATTTAT 47863
QY 7705 AAGATATACATATATATAAGCATACATTTTATGATATATAGAAATATACAGGCGCGGT 7764
DB AAGATATACATATATAAGCATACATTTTATGATATATAGAAATATACAGGCGCGGT 47923
QY 7765 GTGGTGGCTTACCTGTATTTCCAGCATTTTGGGAGGCTGAGGCGGATCACTCA 7824
DB GTGGTGGCTTACCTGTATTTCCAGCATTTTGGGAGGCTGAGGCGGATCACTCA 47983
QY 7825 GGTCAAAAGTTCCGAGCAGCTGCTTACATTTGTCAAAACCGGTTTCTACAAAAATTA 7884
DB GGTCAAAAGTTCCGAGCAGCTGCTTACATTTGTCAAAACCGGTTTCTACAAAAATTA 48043
QY 7885 GCCGGCATGTTGGCAGCAGCTGTATCCAGCTACTCGGAGGCTGAGGCTGAGGCTGAGGAT 7944
DB GCCGGCATGTTGGCAGCAGCTGTATCCAGCTACTCGGAGGCTGAGGCTGAGGCTGAGGAT 48103
QY 7945 CCCTTCAACCCAGGAGCGGAGTGTAGGAGCCCAAGATCGTGCCATTTGCACCTCCAGCT 8004
DB CCCTTCAACCCAGGAGCGGAGTGTAGGAGCCCAAGATCGTGCCATTTGCACCTCCAGCT 48163
QY 8005 TGCGCAATTAAGAGCAAACTCGCTCTCAAAAAAGAAAAAGAAATATACATATAGCGG 8064
DB TGCGCAATTAAGAGCAAACTCGCTCTCAAAAAAGAAAAAGAAATATACATATAGCGG 48223
QY 8065 GCGGTGGTGCATCTGTATCCACCTTTTGGGAGGCTGAGGCGGCGGATCACC 8124
DB GCGGTGGTGCATCTGTATCCACCTTTTGGGAGGCTGAGGCGGCGGATCACC 48283
QY 8125 TGAGTCCAGGAGTTGGAGCAGCAGCTGACTTAACATGGAGAAACCCCATCTCTACTAAAAA 8184
DB TGAGTCCAGGAGTTGGAGCAGCAGCTGACTTAACATGGAGAAACCCCATCTCTACTAAAAA 48343
QY 8185 TACAAAATTAAGCAGCTGGTGACATGCTGTATCCAGCTACTCGGAGGCGTCAAG 8244
DB TACAAAATTAAGCAGCTGGTGACATGCTGTATCCAGCTACTCGGAGGCGTCAAG 48403
QY 8245 GCAGGAGATCGCTTTGAACCTGGGAGGAGGTTGCGGTGAGGCGGAGATCGCGCGGTG 8304

DB 48404 GCAGGAGATCGCTTGAACCTGGGAGGAGGTTGCGGTGAGCGGAGATCGCGCGGTG 48463
QY 8305 CGCTCCATCTCGGCGCAACAGCGCAACCTCCATCTCAAAAAAGAAATATACACATA 8364
DB CGCTCCATCTCGGCGCAACAGCGCAACCTCCATCTCAAAAAAGAAATATACACATA 48523
QY 8365 GCATATAGAAATATACATACATATATAAATATATAGAAATATACATACGTCACACATAT 8424
DB GCATATAGAAATATACATACATATATAAATATATAGAAATATACATACGTCACACATAT 48583
QY 8425 ATACATTCATCTATGTTTAACTTTCTTTATAGGTTTCTCTCCCTCTCTTTTTTTTCT 8484
DB ATACATTCATCTATGTTTAACTTTCTTTATAGGTTTCTCTCCCTCTCTTTTTTTTCT 48643
QY 8485 TTGCAATATATTTTAAAGAAACCGCGCGGTCAGTGCCTCATACCTGTATATCCAGCA 8544
DB TTGCAATATATTTTAAAGAAACCGCGCGGTCAGTGCCTCATACCTGTATATCCAGCA 48703
QY 8545 TTTTGGAGGCGCGAGGTGGGCGGATCACCTGAGGTGAGGATTTGCAACCGGCTTGCCCA 8604
DB TTTTGGAGGCGCGAGGTGGGCGGATCACCTGAGGTGAGGATTTGCAACCGGCTTGCCCA 48763
QY 8605 GCATGTGAACCTTCTCTCTATTAATAAGAAAAATTTAGCTGGGTGTTGATGTGG 8664
DB GCATGTGAACCTTCTCTCTATTAATAAGAAAAATTTAGCTGGGTGTTGATGTGG 48823
QY 8665 CCGTGAATCCAGCTACTCAGGAGGCTGAGGAGGATCGCTTCAACCCAGGAGGCGAG 8724
DB CCGTGAATCCAGCTACTCAGGAGGCTGAGGAGGATCGCTTCAACCCAGGAGGCGAG 48883
QY 8725 AGTTCAGTGCAGCGAGATTCGACCACTGCACTCCAGCTGGGTGACAGCGAGATTC 8784
DB AGTTCAGTGCAGCGAGATTCGACCACTGCACTCCAGCTGGGTGACAGCGAGATTC 48943
QY 8785 TATCTCAAAAAAAGAAAAAAG 8840
DB TATCTCAAAAAAAGAAAAAAG 49003
QY 8841 ACTGTAGATTTTCCAGCTCTAGATTCGATATCTGTGTATTTTCAACATGTTCCCT 8900
DB ACTGTAGATTTTCCAGCTCTAGATTCGATATCTGTGTATTTTCAACATGTTCCCT 49063
QY 8901 ATTCCTCTATTTCTTATAACTTGTAGTGTAGATCTAGAGCTTGTAGGATTCATAAT 8960
DB ATTCCTCTATTTCTTATAACTTGTAGTGTAGATCTAGAGCTTGTAGGATTCATAAT 49123
QY 8961 GATGTTCTGTAGGATTTTATGCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 9020
DB GATGTTCTGTAGGATTTTATGCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 49183
QY 9021 ATGCTGTGTTTCTCTTTTGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 9080
DB ATGCTGTGTTTCTCTTTTGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 49243
QY 9081 GTTATTTAATGAGGTTGATATAATCTGATAATCTAATTTCTATCATTTTATTTATTCAT 9140
DB GTTATTTAATGAGGTTGATATAATCTGATAATCTAATTTCTATCATTTTATTTATTCAT 49303
QY 9141 TAGGATATTTCTTAAATAGAACTTCCCTCATCAATTTGATGATATATTTGGGAGCA 9200
DB TAGGATATTTCTTAAATAGAACTTCCCTCATCAATTTGATGATATATTTGGGAGCA 49363
QY 9201 GTTCACAGAGAAAGGATATAAATGCTGATTTTCTATTTTCTATTTTCTATTTTCTAT 9260
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QY 9261 TAAAGAGTGTGTTCTGTAGCATCTTCAAGGTGAAATGAACTTTTGTGTTGTTGT 9320
DB TAAAGAGTGTGTTCTGTAGCATCTTCAAGGTGAAATGAACTTTTGTGTTGTTGT 49483
QY 9321 TGTCCAGATTTCTTAAATGTCTCCCTTCAAGGAGGATTTGTTGTTGTTGTTGTTGTTGTTG 9380
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Db 45105 GTGGGCTCTGAGGTGAATTTATGCACACGCCGCCCAAGGGGCTTAGAAGGCCGGGACCC 45164
OY 5005 GAGAGGTTAGCTGGGGGCGGGGTAGAGCCCGCTGACCCGAGGGCGCGGGCGGAGGACT 5064
Db 45165 GAGAGGTTAGCTGGGGGCGGGGTAGAGCCCGCTGACCCGAGGGCGCGGGCGGAGGACT 45224
OY 5065 GCGGCTCCCGGCGGTTGGGGCGGGCGGCTCCCGGCTCGGAGACTGGCGCGGAGACT 5124
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OY 5365 AAGAGCGAGCGAGGGGTAGGAGATTGCACACTGGGCTGGAGGGCGCTGGAGGTC 5424
Db 45525 AAGAGCGAGCGAGGGGTAGGAGATTGCACACTGGGCTGGAGGGCGCTGGAGGTC 45584
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OY 5785 TCCCGTTTCCAAATTAATTTATTTAAAGCGGGGATTTATTTACCTCAGAGCT 5844
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OY 5845 AGATTAATGATTTATTTTAAATATTTGATTTATGATTTATGATTTGATTTGAT 5904
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Db 46125 GCGTAGAAGATTAATGCTGATTTCAAGAGCGCTTATTTGAGCTTGTGTTACCTAAA 46184
OY 6025 TTGCGTTTCCAGACTCAAGAGAGATTTAGTTTACTGCTTGGATTTGATTTGAT 6084
Db 46185 TTGCGTTTCCAGACTCAAGAGAGATTTAGTTTACTGCTTGGATTTGATTTGATTTGAT 46244

OY 6085 TCATAGTGCATATATTAATTTCAAGCAATCCAGCACTTGGAGGCTTAAGCGCGC 6144
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OY 6745 GGTAGGCGCTTGGGCTGTTATATTTATTTATTTATTTATTTATTTATTTATTTAT 6804
Db 46904 GGTAGGCGCTTGGGCTGTTATATTTATTTATTTATTTATTTATTTATTTATTTATTT 46963
OY 6805 TGAATTCAGGCGCTGAGAACTAAGAGATAGACTTGGCATCTAGGCTTACTTTAAG 6864
Db 46964 TGAATTCAGGCGCTGAGAACTAAGAGATAGACTTGGCATCTAGGCTTACTTTAAG 47023
OY 6865 TCACTACGATTAATCACTCAACACACCCCTCTCTAGGTTTATTTGCGACCTT 6924
Db 47024 TCACTACGATTAATCACTCAACACACCCCTCTCTAGGTTTATTTGCGACCTT 47083
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Db 47084 TTAATCTGCTTTATAGAAATTTTCAACGCTATCAACCGTAGAAGAGATGTAATG 47143
OY 6985 AACCATCACTTACTTCAACTACAGTTGAATATCTGCTGCTGCTGCTGCTGCTGCTG 7044
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OY 7045 GAAGCGTTTGAATTTCAATTCATTTTGGATTTGGAAATTTGCAATACATTAATGAG 7104
Db 47204 GAAGCGTTTGAATTTCAATTCATTTTGGATTTGGAAATTTGCAATACATTAATGAG 47263
OY 7105 ATATCTTGGGAGGAGCCAGTCTAAACATGAATTCAGTTATATTTATTTATTTAT 7164
Db 47264 ATATCTTGGGAGGAGCCAGTCTAAACATGAATTCAGTTATATTTATTTATTTATTT 47323

Db	68308	AAAGACTGCTTACCTTGGCCAAATATCATTTATGATTAATATATATGACAAAGCTTTAG	68365
QY	28921	ACAGTGTCTGATGATATAATAAATTCCTATTAATTAATGTTAACTTACTTCCTGTTCCCTGCC	28980
Db	68368	ACAGTGTCTGATGATATAATAAATTCCTATTAATTAATGTTAACTTACTTCCTGTTCCCTGCC	68422
QY	28981	CCAAATACACAACTGCTAGATGCAACATTAAGCTATATGAGACCTGGATAGCTGTTGT	29040
QY	29041	TCATTACTGATATCCCTGGTGGCCGCACATATGGACATATGACATATGACACTAAATTAAGAT	29100
Db	68488	TCATTACTGATATCCCTGGTGGCCGCACATATGAGACATATGACACTAAATTAAGAT	68547
QY	29101	TTGTTGAATGAATGATGATGATGCTCTTCTTGCAAGCTTACCTTGAACCTGATGAGC	29160
Db	68548	TTGTTGAATGAATGATGATGATGCTCTTCTTGCAAGCTTACCTTGAACCTGATGAGC	68607
QY	29161	TGCGCATACCTTATGATGCTGGGAAAAAGATATAAAAGCTTCATCTCTGTCGACACATC	29220
Db	68608	TGCGCATACCTTATGATGCTGGGAAAAAGATATAAAAGCTTCATCTCTGTCGACACATC	68667
QY	29221	TTTTCTTGTGTTGATGTAGATGCTTCACCTCAGCCCTCATCAGATTAATTAACAGGA	29280
Db	68668	TTTTCTTGTGTTGATGTAGATGCTTCACCTCAGCCCTCATCAGATTAATTAACAGGA	68722
QY	29281	GAAGGAGAGGACGATGGGTGATCCAAATGAAGAAAGCACTGCTCTTTCGACAGCTTTT	29340
Db	68728	GAAGGAGAGGACGATGGGTGATCCAAATGAAGAAAGCACTGCTCTTTCGACAGCTTTT	68787
QY	29341	TCCACAGACAGATAGCTCAGATTCCTGGGAATTTGGGAAGCCGTGGCTTTTATATA	29400
Db	68788	TCCACAGACAGATAGCTCAGATTCCTGGGAATTTGGGAAGCCGTGGCTTTTATATA	68844
QY	29401	AATCAAAATAACTGATATCTTAAAGGCTTTCGACCTTTTCTGAGAAATCTTGACATGAT	29460
Db	68848	AATCAAAATAACTGATATCTTAAAGGCTTTCGACCTTTTCTGAGAAATCTTGACATGAT	68907
QY	29461	TTGAGTCTCATATTTGCTAGTAAGCAAAATTAATTAAGCTTTGCTGAGAAAGGATTAAT	29520
Db	68908	TTGAGTCTCATATTTGCTAGTAAGCAAAATTAATTAAGCTTTGCTGAGAAAGGATTAAT	68967
QY	29521	AAGGCAAGAATATGAAGCTATTTAATATCATTTAATAGAGAAATGCCAATCAAAACCAT	29580
Db	68968	AAGGCAAGAATATGAAGCTATTTAATATCATTTAATAGAGAAATGCCAATCAAAACCAT	69027
QY	29581	GTCGACACCCATTAAATGATCACTTTATTCGAAAAAACCAGACAGCTATGACAAATGT	29640
Db	69028	GTCGACACCCATTAAATGATCACTTTATTCGAAAAAACCAGACAGCTATGACAAATGT	69087
QY	29641	GGAGAAATTTGAAAACTTGTGTACTATTTGCTGGAATGTTAAATAGTGCAGCTGCCAGG	29700
Db	69088	GGAGAAATTTGAAAACTTGTGTACTATTTGCTGGAATGTTAAATAGTGCAGCTGCCAGG	69147
QY	29701	AAAGTATGATGGCTCCCTCAAAAAATTTAAAAATAGAGCCAGGACGGTGAATCTCTGAGG	29760
Db	69148	AAAGTATGATGGCTCCCTCAAAAAATTTAAAAATAGAGCCAGGACGGTGAATCTCTGAGG	69207
QY	29761	TCAGAGATTTGAGACACAGCTGACCAAAATGTTGAAAAACCCGCTCTACTAAATACAAA	29820
Db	69208	TCAGAGATTTGAGACACAGCTGACCAAAATGTTGAAAAACCCGCTCTACTAAATACAAA	69267
QY	29821	AATTAGCTGGGCATGCTGGCCATATGCTGTATATCCAGCTACTTGGAGGCTGAGCAGG	29880
Db	69268	AATTAGCTGGGCATGCTGGCCATATGCTGTATATCCAGCTACTTGGAGGCTGAGCAGG	69322
QY	29881	AGAAATTCCTTGAACCCGGAGGAGAGAGTGTATGTAAGCCGATATATCCATATGACATC	29940
Db	69328	AGAAATTCCTTGAACCCGGAGGAGAGAGTGTATGTAAGCCGATATATCCATATGACATC	69387
QY	29941	CAACCTTGCGCACAGAAACAAAACCTCGCTCAAAATTAATTAATTAATTAATGAATGAC	30000

[illegible]

QY 23401 GATGGTTTGAGGAAGAGGAGGAGGAAGAAATGACAGATGAGTCTGAGCAAGAT 23460
DB 62848 GATGGTTTGAGGAAGAGGAGGAGGAGGAAGAAATGACAGATGAGTCTGAGCAAGAT 62907
QY 23461 GGAGAAAGAAAGGTAGAGAAAGAAAGAAAGAAAGAAAGTAAAGAGAGAGAGAGAGAA 23520
DB 62908 GGAGAAAGAAAGGTAGAGAAAGAAAGAAAGAAAGAAAGTAAAGAGAGAGAGAGAA 62967
QY 23521 GAAG 23580
DB 62968 GAAG 63027
QY 23581 CCTTCATGAGTAAATAG 23640
DB 63028 CCTTCATGAGTAAATAG 63087
QY 23641 TCAATTTGATAG 23700
DB 63088 TCAATTTGATAG 63147
QY 23701 CTTAGCAAGCTGAGTGTGTCAGTACAGTAAATCTGATGATCATATATATATCTG 23760
DB 63148 CTTAGCAAGCTGAGTGTGTCAGTACAGTAAATCTGATGATCATATATATATCTG 63207
QY 23761 AATACAGATATTCAGTGTGTCAGTACAGTAAATCTGATGATCATATATATATCTG 23820
DB 63208 AATACAGATATTCAGTGTGTCAGTACAGTAAATCTGATGATCATATATATATCTG 63267
QY 23821 ATTTAATATATAATATCTGATGATCATATATATATCTGATGATCATATATATCTG 23880
DB 63268 ATTTAATATATAATATCTGATGATCATATATATATCTGATGATCATATATATCTG 63327
QY 23881 TGTGTTTATATAGTGTGTCAGTACAGTAAATCTGATGATCATATATATATCTG 23940
DB 63328 TGTGTTTATATAGTGTGTCAGTACAGTAAATCTGATGATCATATATATATCTG 63387
QY 23941 GGCCTGAGTAAATCTGATGATCATATATATATCTGATGATCATATATATCTG 24000
DB 63388 GGCCTGAGTAAATCTGATGATCATATATATATCTGATGATCATATATATCTG 63447
QY 24001 AAGAAGGATTTGTAAG 24060
DB 63448 AAGAAGGATTTGTAAG 63507
QY 24061 GAAAGACAGTATGATGATCATATATATATCTGATGATCATATATATCTG 24120
DB 63508 GAAAGACAGTATGATGATCATATATATCTGATGATCATATATATCTG 63567
QY 24121 GGTGGCTCATGCTGATGATCATATATCTGATGATCATATATCTGATGATCATATAT 24180
DB 63568 GGTGGCTCATGCTGATGATCATATATCTGATGATCATATATCTGATGATCATATAT 63627
QY 24181 TCAGAGAGTGTAG 24240
DB 63628 TCAGAGAGTGTAG 63687
QY 24241 AAATAGCTGTGTGAG 24300
DB 63688 AAATAGCTGTGTGAG 63747
QY 24301 TTGAAGCTGGGAG 24360
DB 63748 TTGAAGCTGGGAG 63807
QY 24361 GCGACAG 24420
DB 63808 GCGACAG 63867
QY 24421 TGCTGAGTACATGATGATGATCATATATATCTGATGATCATATATATCTG 24480
DB 63868 TGCTGAGTACATGATGATGATCATATATATCTGATGATCATATATATCTG 63927
QY 24481 GGTCTCATGATGATGATGATCATATATCTGATGATCATATATATCTG 24540

DB 63928 GGTCTCATGATGATGATGATCATATATCTGATGATCATATATATCTG 63987
QY 24541 TTGGGCTCCCAAG 24600
DB 63988 TTGGGCTCCCAAG 24660
QY 24601 TATTTATTTATTTGAG 24660
DB 64048 TATTTATTTATTTGAG 64107
QY 24661 AGTGTGCTGAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 24720
DB 64108 AGTGTGCTGAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 64167
QY 24721 CTTAGCTGCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 24780
DB 64168 CTTAGCTGCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 64227
QY 24781 GGTAGAGGTAAAG 24840
DB 64228 GGTAGAGGTAAAG 64287
QY 24841 GATATGCTATATGAG 24900
DB 64288 GATATGCTATATGAG 64347
QY 24901 AACCAATGAGCATATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24960
DB 64348 AACCAATGAGCATATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64407
QY 24961 TTTTGTGTTGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 25020
DB 64408 TTTTGTGTTGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64467
QY 25021 AATGAG 25080
DB 64468 AATGAG 64527
QY 25081 TGGCAAGGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 25140
DB 64528 TGGCAAGGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64587
QY 25141 TCTGTTAAG 25200
DB 64588 TCTGTTAAG 64647
QY 25201 TTGGCTTGATTTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 25260
DB 64648 TTGGCTTGATTTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64707
QY 25261 TTATTTGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 25320
DB 64708 TTATTTGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64767
QY 25321 CAGCCTAGCAAAAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 25380
DB 64768 CAGCCTAGCAAAAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64827
QY 25381 TCAGCTTGATTTAAG 25440
DB 64828 TCAGCTTGATTTAAG 64887
QY 25441 TTCCAGTTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25500
DB 64888 TTCCAGTTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 64947
QY 25501 ATTTTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 25560
DB 64948 ATTTTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 65007
QY 25561 GATGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 25620

Db	60628	AGTATCTCTGGCATGATTACCGTTAGCACACCTAGAGGTGGGGTGACAGCTGGCT	60687
QY	21241	TTATTTTATTTTATAGATATCATTTGTCTTATATATAAAACCCCATTTATAGACAAATATA	21300
Db	60688	TTATTTTATTTTATAGATATCATTTGTCTTATATATAAAACCCCATTTATAGACAAATATA	60747
QY	21301	TAGATAAATGAAAACTTAACTCTCTATACAGACAGGTTCTATAACCATATCTGTAT	21360
Db	60748	TAGATAAATGAAAACTTAACTCTCTATACAGACAGGTTCTATAACCATATCTGTAT	60807
QY	21361	CTTTTAAACTCTCTTTTGGACATATGTATATATATTAATTTAAACAAACAGGCTGGGT	21420
Db	60808	CTTTTAAACTCTCTTTTGGACATATGTATATATATTAATTTAAACAAACAGGCTGGGT	60867
QY	21421	CGATGGGCACATCGCTGTAACTTAGCAGCTTTGGAGGACAGGAGGATCTGTGA	21480
Db	60868	CGATGGGCACATCGCTGTAACTTAGCAGCTTTGGAGGACAGGAGGATCTGTGA	60927
QY	21481	GCTCAGGAGTTGGAGACACCGCTGGCAACATAGTGAGCCCTCATCTCTACCAAAANAA	21540
Db	60928	GCTCAGGAGTTGGAGACACCGCTGGCAACATAGTGAGCCCTCATCTCTACCAAAANAA	60987
QY	21541	AAAATATCCAGGCATGTGGCTGCACCTGTGGCCCCAGATCTTGGGAGCTGAGACA	21600
Db	60988	AAAATATCCAGGCATGTGGCTGCACCTGTGGCCCCAGATCTTGGGAGCTGAGACA	61047
QY	21601	GGAGCATCTTTGAGCCAGGAGTTGAGGTTGATAGTATGTGGCAGCTGCACCT	21660
Db	61048	GGAGCATCTTTGAGCCAGGAGTTGAGGTTGATAGTATGTGGCAGCTGCACCT	61107
QY	21661	CCAGCCTAGGCGAGAGTGAGACCCCTGTCTCAAAACAAACCCCAAAACAAACACC	21720
Db	61108	CCAGCCTAGGCGAGAGTGAGACCCCTGTCTCAAAACAAACCCCAAAACAAACACC	61167
QY	21721	CACCTATATGTGATCAATCAATGATCTCTCTTTTGTCTTTTGTGAAATGTATTAAGGACA	21780
Db	61168	CACCTATATGTGATCAATCAATGATCTCTCTTTTGTCTTTTGTGAAATGTATTAAGGACA	61227
QY	21781	GCTCTCACCCCTCCCTGAAATCACAAGTATATATATCATGAGGAAACAGTTTAAACAC	21840
Db	61228	GCTCTCACCCCTCCCTGAAATCACAAGTATATATATCATGAGGAAACAGTTTAAACAC	61287
QY	21841	TGAAAAAGGTATCAAAATGAAAACTAGTCTTCCCAAGATTAACATTAACAAATTTCTTG	21900
Db	61288	TGAAAAAGGTATCAAAATGAAAACTAGTCTTCCCAAGATTAACATTAACAAATTTCTTG	61347
QY	21901	TATGTCTTTATAGGAGTATTTTATCCATATACCGTATTTTGTGAATGTGTGACATG	21960
Db	61348	TATGTCTTTATAGGAGTATTTTATCCATATACCGTATTTTGTGAATGTGTGACATG	61407
QY	21961	AACATTTACTCCCTCTCAGGANTCTCTAGTGCTTTTATATGTTTATCTCATTTAATC	22020
Db	61408	AACATTTACTCCCTCTCAGGANTCTCTAGTGCTTTTATATGTTTATCTCATTTAATC	61467
QY	22021	CTTACACCCCTATAGAGTAAATAGATAGTATCTCTTATTTGTATATGAAGAACTGAT	22080
Db	61468	CTTACACCCCTATAGAGTAAATAGATAGTATCTCTTATTTGTATATGAAGAACTGAT	61527
QY	22081	ATGCAGACACTTAAGACACTTGTCAAGTTTACAGCTAATAAATGGTAGGACAGTA	22140
Db	61528	ATGCAGACACTTAAGACACTTGTCAAGTTTACAGCTAATAAATGGTAGGACAGTA	61587
QY	22141	GTCATATCCAGACCACTTAACCTCCAGAGCTCAGATCTACTTATATGCTTTTGGAGCTT	22200
Db	61588	GTCATATCCAGACCACTTAACCTCCAGAGCTCAGATCTACTTATATGCTTTTGGAGCTT	61647
QY	22201	TTTTTTTTTTTTTTTTTTTTTCTCTTAAGACAGAGTCTCTGCAGCTGTCAACCTGGCTGGAGT	22260
Db	61648	TTTTTTTTTTTTTTTTTTTTTCTCTTAAGACAGAGTCTCTGCAGCTGTCAACCTGGCTGGAGT	61707
QY	22261	GCAATGGCAGCATTTAGCTCAGTCAACCTCTACCTCTCGGTTTCAAGTGATTTCTCTG	22320
Db	61708	GCAATGGCAGCATTTAGCTCAGTCAACCTCTACCTCTCGGTTTCAAGTGATTTCTCTG	61767
QY	22321	CCTAGCCTCCGAATAGCTGGGATTTACAGGTGCTTGCACCATGCTCTGCTAAATTTTG	22380
Db	61768	CCTAGCCTCCGAATAGCTGGGATTTACAGGTGCTTGCACCATGCTCTGCTAAATTTTG	61827
QY	22381	TATTTTATAGTAGAGTGAAGTTTCGCTATGTTGGCCAGGCTGCTCTCGAACTCCIGACCT	22440
Db	61828	TATTTTATAGTAGAGTGAAGTTTCGCTATGTTGGCCAGGCTGCTCTCGAACTCCIGACCT	61887
QY	22441	CTGTATCTGCCACCTTGGCCCGCAAGCTGCTGGGATTTACAGGCGTGAAGTCACTGGCC	22500
Db	61888	CTGTATCTGCCACCTTGGCCCGCAAGCTGCTGGGATTTACAGGCGTGAAGTCACTGGCC	61947
QY	22501	CGGCCCTGAGGCTTTTAAATGGCTGCATAATATTCCATTGAATGAATACAACATGA	22560
Db	61948	CGGCCCTGAGGCTTTTAAATGGCTGCATAATATTCCATTGAATGAATACAACATGA	62007
QY	22561	CTCATTAACCATCTCGTATTTGACAGATGTCTGTTGTTCCAGTTGTTGCTATTCAGT	22620
Db	62008	CTCATTAACCATCTCGTATTTGACAGATGTCTGTTGTTCCAGTTGTTGCTATTCAGT	62067
QY	22621	ACAGTGTATATATAGTCCAGATATATGGTGTATATAGATGAAATTCCTTACAGT	22680
Db	62068	ACAGTGTATATATAGTCCAGATATATGGTGTATATAGATGAAATTCCTTACAGT	62127
QY	22681	GGATTTGTCATGATATATACATTTTGATATATATATCATCCAGTGTCTTTCAGAAATGG	22740
Db	62128	GGATTTGTCATGATATATACATTTTGATATATATATCATCCAGTGTCTTTCAGAAATGG	62187
QY	22741	TGTGACCACTCTGAATCAGGTATAGTTCCTGTTCCCTCAATAGGTATATCAAA	22800
Db	62188	TGTGACCACTCTGAATCAGGTATAGTTCCTGTTCCCTCAATAGGTATATCAAA	62247
QY	22801	CCTTCTAAATTTTGGCAGGCTAAACATGTGCAAAATGTATCTGTTATTTGATTTGTAGC	22860
Db	62248	CCTTCTAAATTTTGGCAGGCTAAACATGTGCAAAATGTATCTGTTATTTGATTTGTAGC	62307
QY	22861	TCTTCAATTTAGAAATGAGATTAAGCATTTTAAATTTTAAATTAATATATATGTTTATTT	22920
Db	62308	TCTTCAATTTAGAAATGAGATTAAGCATTTTAAATTTTAAATTAATATATATGTTTATTT	62367
QY	22921	TTCTGGAATCTCCAGCTCATATCATTTACTCGAGTCTGTTCTCTTTCTTTCTTT	22980
Db	62368	TTCTGGAATCTCCAGCTCATATCATTTACTCGAGTCTGTTCTCTTTCTTTCTTT	62427
QY	22981	TAAATAGTAAATTTATCAATGTTTCTTTCATGGCTTTTGGAGCCACAGACTTCAAGCT	23040
Db	62428	TAAATAGTAAATTTATCAATGTTTCTTTCATGGCTTTTGGAGCCACAGACTTCAAGCT	62487
QY	23041	CTACTCCCTACCCAGCTTTTCTCTTTTGAACAAATTTTATTAATCCCTGAGTAGTAT	23100
Db	62488	CTACTCCCTACCCAGCTTTTCTCTTTTGAACAAATTTTATTAATCCCTGAGTAGTAT	62547
QY	23101	ACTATCTAGGTTGCAAGAGTTCTCTTCTGATCTCAATTAATAATACTCTCTGTTCT	23160
Db	62548	ACTATCTAGGTTGCAAGAGTTCTCTTCTGATCTCAATTAATAATACTCTCTGTTCT	62607
QY	23161	AAATAACAAAAGCCCAAGATTAAGTCTGAGAGTCTGAGATTTTCTTTTGGATGTGACTAGA	23220
Db	62608	AAATAACAAAAGCCCAAGATTAAGTCTGAGAGTCTGAGATTTTCTTTTGGATGTGACTAGA	62667
QY	23221	ATATTTCTGGAGTTGCCCTAAAATGATACCTTAATTTATTTATTTGCTTAAAGCAATTTCT	23280
Db	62668	ATATTTCTGGAGTTGCCCTAAAATGATACCTTAATTTATTTATTTGCTTAAAGCAATTTCT	62727
QY	23281	ACATATTTCTGTTGAGGTGAAGGCTTCAGGTGTTTAAAGCTTAAACTGCAAGAGCAATG	23340
Db	62728	ACATATTTCTGTTGAGGTGAAGGCTTCAGGTGTTTAAAGCTTAAACTGCAAGAGCAATG	62787
QY	23341	AAACTCCCAAGGTTTGGAGGCGCCAGAGCGCCAGGACCTGTTTAAATTAAGTAATGAA	23400
Db	62788	AAACTCCCAAGGTTTGGAGGCGCCAGAGCGCCAGGACCTGTTTAAATTAAGTAATGAA	62847

OY	19021	GAGCTGTGATCGACCCAGCTGCACTCCAGCTTGACGACAGAGAGACCCCTGTCTTAA	19080
Db	58468	GAGCTGTGATCGACCCAGCTGCACTCCAGCTTGACGACAGAGAGACCCCTGTCTTAA	58527
OY	19081	AAGACAATGAAAAAGTGGCTGGGACAAATGGCTCACACCTGTAAACCTTGGACTTGGGA	19140
Db	58528	AAGACAATGAAAAAGTGGCTGGGACAAATGGCTCACACCTGTAAACCTTGGACTTGGGA	58587
OY	19141	GGCTGAGGAGGTGGATCATTTCAATGTCAGAGAGTTGACAGCAGCTGGACAACATGGCA	19200
Db	58588	GGCTGAGGAGGTGGATCATTTCAATGTCAGAGAGTTGACAGCAGCTGGACAACATGGCA	58647
OY	19201	AAACCGGTCTCTCAAAAAATACAAAAATCGGCACTGGCAGTGGCTCACTCTGTATTC	19260
Db	58648	AAACCGGTCTCTCAAAAAATACAAAAATCGGCACTGGCAGTGGCTCACTCTGTATTC	58707
OY	19261	TCAGCACTTTGGAGGCCAGAGTGGGTGGATCATCTGAGATCAGAGAGTTCAAGACAGCC	19320
Db	58708	TCAGCACTTTGGAGGCCAGAGTGGGTGGATCATCTGAGATCAGAGAGTTCAAGACAGCC	58767
OY	19321	TGGCCAAATGAGTGAACCCCATCTCTACTAAAAATAAAAATTAAGCTGGGTG	19380
Db	58768	TGGCCAAATGAGTGAACCCCATCTCTACTAAAAATAAAAATTAAGCTGGGTG	58827
OY	19381	TGGTACGCACTGCTCTAATCCAGCTTCTAGAGAGGCTGAGGAGAAATTTGTTGA	19440
Db	58828	TGGTACGCACTGCTCTAATCCAGCTTCTAGAGAGGCTGAGGAGAAATTTGTTGA	58887
OY	19441	CCCAGAGGTGAGGTTTACAGTGAAGCCAGATCCACCTGCTGGCTGGGCAAC	19500
Db	58888	CCCAGAGGTGAGGTTTACAGTGAAGCCAGATCCACCTGCTGGCTGGGCAAC	58947
OY	19501	AAGAGTAGACTCCGCTCTCAAAAAATTAAGTGAATATGGTGGTACATGC	19560
Db	58948	AAGAGTAGACTCCGCTCTCAAAAAATTAAGTGAATATGGTGGTACATGC	59007
OY	19561	CTATAGTCTGGCTATCTCAGAGAGGCTGAGTGAAGATCACTTAAGTTGGGAGA	19620
Db	59008	CTATAGTCTGGCTATCTCAGAGAGGCTGAGTGAAGATCACTTAAGTTGGGAGA	59067
OY	19621	TTGAGGCTACAGTGAAGCAAGATTGCAACCACTCCAGCTTGGCCGCAAAAGCGA	19680
Db	59068	TTGAGGCTACAGTGAAGCAAGATTGCAACCACTCCAGCTTGGCCGCAAAAGCGA	59127
OY	19681	GACTCCATTAAAAATAACCATTTATCATGAGAGAGAGCGCCCTGAAATATTCAG	19740
Db	59128	GACTCCATTAAAAATAACCATTTATCATGAGAGAGAGCGCCCTGAAATATTCAG	59187
OY	19741	TGTGATCACTCCAAAGAACTTCTCCTTAAAACTCCAGCTCTCATCAAGATTGCA	19800
Db	59188	TGTGATCACTCCAAAGAACTTCTCCTTAAAACTCCAGCTCTCATCAAGATTGCA	59247
OY	19801	TTATGATATGAAGTGTAAAGAGTGAAGGATTTGCTCCAGTAAAGCTTAATTCAGT	19860
Db	59248	TTATGATATGAAGTGTAAAGAGTGAAGGATTTGCTCCAGTAAAGCTTAATTCAGT	59307
OY	19861	GGGAGAGAAATTTCTAAGATATTGCACTGGGAGAGAGGTTAATTATCACTAATG	19920
Db	59308	GGGAGAGAAATTTCTAAGATATTGCACTGGGAGAGAGGTTAATTATCACTAATG	59367
OY	19921	GATTGCTCACTCTGCTGCTCCAGATATATATTTCCGTTTGTATCAAGTTGACAT	19980
Db	59368	GATTGCTCACTCTGCTGCTCCAGATATATATTTCCGTTTGTATCAAGTTGACAT	59427
OY	19981	GTGGTACTGGGCTGCAATATTTCTTCTCATGTGACCAATGTACTAGTGAAGTT	20040
Db	59428	GTGGTACTGGGCTGCAATATTTCTTCTCATGTGACCAATGTACTAGTGAAGTT	59487
OY	20041	TTTCAAAAAAATTTTACAGTCTGCTGCTTATGTTATATCACTGACTGATTTGAT	20100
Db	59488	TTTCAAAAAAATTTTACAGTCTGCTGCTTATGTTATATCACTGACTGATTTGAT	59547
OY	20101	TTATTTCCCTTTTGAATAAATTTGACTTGCCTATATTAGTAATTCGCAATATATG	20160

Db	59548	TTATTTCCCTTTTGAATAAATTTGACTTGCCTATATTAGTAATTCGCAATATATG	59607
OY	20161	AAACATTCAAAAATAGGAATTTGATCCAGCATTTGGAGGCGCAAGTGGGCTGATCAT	20220
Db	59608	AAACATTCAAAAATAGGAATTTGATCCAGCATTTGGAGGCGCAAGTGGGCTGATCAT	59667
OY	20221	TTGAGGTAGAGATTTCAGACACACCTGGCTTACATGGTGAAACCTGTCTACTTAA	20280
Db	59668	TTGAGGTAGAGATTTCAGACACACCTGGCTTACATGGTGAAACCTGTCTACTTAA	59727
OY	20281	ATACAAAAAATTAAGTGGGAGTGGTGGCTGCTGCTGTAACCTCACTACTGAGAGAC	20340
Db	59728	ATACAAAAAATTAAGTGGGAGTGGTGGCTGCTGCTGTAACCTCACTACTGAGAGAC	59787
OY	20341	TGAGGAGAGAAATCGCTTGAACCTTGAGATGAGAGTTGCACTGAGCTGATCAGATC	20400
Db	59788	TGAGGAGAGAAATCGCTTGAACCTTGAGATGAGAGTTGCACTGAGCTGATCAGATC	59847
OY	20401	ACTGCACTCCAGCCTGGGCAATAGAGTGAAGTCACTGCTCAAAAACAAAAACAG	20460
Db	59848	ACTGCACTCCAGCCTGGGCAATAGAGTGAAGTCACTGCTCAAAAACAAAAACAG	59907
OY	20461	CAATTAACAAATAGGAATTTTAAAAAGAGACCAAAACCATGAAAAATTAAGCCCTTGA	20520
Db	59908	CAATTAACAAATAGGAATTTTAAAAAGAGACCAAAACCATGAAAAATTAAGCCCTTGA	59967
OY	20521	TGAGTGAATTAATATCTTTTCTTCTCACTGCTTAATTAATTAAGAAATTTTAAAGA	20580
Db	59968	TGAGTGAATTAATATCTTTTCTTCTCACTGCTTAATTAATTAAGAAATTTTAAAGA	60027
OY	20581	TGTTCAAAAGAAATTCACATATTTAGAAATTTAGATTAATTTCTGCTGATTTTAA	20640
Db	60028	TGTTCAAAAGAAATTCACATATTTAGAAATTTAGATTAATTTCTGCTGATTTTAA	60087
OY	20641	AAGTCTATTTTGAACCTTTGAGAGAAAGAACAGTTGCGCAGTAAATTTTAAAGAA	20700
Db	60088	AAGTCTATTTTGAACCTTTGAGAGAAAGAACAGTTGCGCAGTAAATTTTAAAGAA	60147
OY	20701	GTTTATGAATTTGACACAGAGTGTAGTACCAAGGGTTTTGTTCTCTGCTATG	20760
Db	60148	GTTTATGAATTTGACACAGAGTGTAGTACCAAGGGTTTTGTTCTCTGCTATG	60207
OY	20761	TGCTTCCCTCATTAATTTGAGCTAAAAAACTTACCTTAATAGCTTAAAGAAAGA	20820
Db	60208	TGCTTCCCTCATTAATTTGAGCTAAAAAACTTACCTTAATAGCTTAAAGAAAGA	60267
OY	20821	GTTTGAAGTGGCAAACTGACACACTGCTGGCTTTGGCTTTAGAACTGAAAGCTTG	20880
Db	60268	GTTTGAAGTGGCAAACTGACACACTGCTGGCTTTGGCTTTAGAACTGAAAGCTTG	60327
OY	20881	AAGCAGGTTTTGGAAGCATGCTAATCCAGAGCCAAACCCAGGCTGTCAGACAGTG	20940
Db	60328	AAGCAGGTTTTGGAAGCATGCTAATCCAGAGCCAAACCCAGGCTGTCAGACAGTG	60387
OY	20941	AATGTAGACTCATTAATGAAAGCATGGGCACTGATGAAAGAGAGCTAAAGCAGAT	21000
Db	60388	AATGTAGACTCATTAATGAAAGCATGGGCACTGATGAAAGAGAGCTAAAGCAGAT	60447
OY	21001	GTGTACTGCTGACTTGAACCTTAAGAAAGTTGATGAGAGCAAGCCACCAAAACAGT	21060
Db	60448	GTGTACTGCTGACTTGAACCTTAAGAAAGTTGATGAGAGCAAGCCACCAAAACAGT	60507
OY	21061	ATTGAGCCCAAGGTTTTGTTTTGCTTTTGTATTTCAATCAAGATCTTCAAG	60567
Db	60508	ATTGAGCCCAAGGTTTTGTTTTGCTTTTGTATTTCAATCAAGATCTTCAAG	60627
OY	21121	CTATTAAAAAATTTATGAAGAAAGTATAGAAATCTTTTCTTGAGAGCTTTGAGAGC	21180
Db	60568	CTATTAAAAAATTTATGAAGAAAGTATAGAAATCTTTTCTTGAGAGCTTTGAGAGC	60627
OY	21181	AGTATCTGCGCATGATTCAGGTAGCACACCTAGAGGTGGGTGCAACAGCTGGCT	21240

Db	55168	ACTCTCCCTTGAGGACAGTATGAAATGCGTGTAAAGACTTAGACCTTGTGACAAAGACAG	55227
Qy	15781	GATTGAATCTCAACACAGCATAGTAATGTCTTAACATTTGTATACGCATTTGACCTCTTC	15840
Db	55228	GATTGAATCTCAACACTAGCATAGTAATGTCTTAACATTTGTATACGCATTTGACCTCTTC	55287
Qy	15841	AAGCATCTTTTGTCTTTAAAAAAGAGAAAGAACCCAGACACAGTGGTGCACACCTGTGTGC	15900
Db	55288	AAGCATCTTTTGTCTTTAAAAAAGAGAAAGAACCCAGACACAGTGGTGCACACCTGTGTGC	55347
Qy	15901	CAGCTACTGGGAGGCTGAGCAGACAAAGGGTCACTTGAACCCAGAGTTTAAAGCCATC	15960
Db	55348	CAGCTACTGGGAGGCTGAGCAGACAAAGGGTCACTTGAACCCAGAGTTTAAAGCCATC	55407
Qy	15961	CTGGGCAGCATATGAAATCTGTCTCAAAAAAAGAAAAAAGAAAAAAGACACTA	16020
Db	55408	CTGGGCAGCATATGAAATCTGTCTCAAAAAAAGAAAAAAGAAAAAAGACACTA	55467
Qy	16021	TATGACTGTGGGCTATGTGAATTTGTTGAAATATGCATGCAAAATGATAGTATTA	16080
Db	55468	TATGACTGTGGGCTATGTGAATTTGTTGAAATATGCATGCAAAATGATAGTATTA	55527
Qy	16081	ACAACTCTCAAAAAAGTTGTGCTGCTCACTATTTATGTAATTTGGTTCACATCAAG	16140
Db	55528	ACAACTCTCAAAAAAGTTGTGCTGCTCACTATTTATGTAATTTGGTTCACATCAAG	55587
Qy	16141	ACTTTTTTTTTTTTGAGACGGGCTTCACTGCTCTTCCACCTAGGCTGAGTGCATGC	16200
Db	55588	ACTTTTTTTTTTTTGAGACGGGCTTCACTGCTCTTCCACCTAGGCTGAGTGCATGC	55647
Qy	16201	TGCGATCTCGGCTCACTGCAACCCCGCCCTCGGGTTCAGCAATTTCTTGCTCAAG	16260
Db	55648	TGCGATCTCGGCTCACTGCAACCCCGCCCTCGGGTTCAGCAATTTCTTGCTCAAG	55707
Qy	16261	CTCTCACTAGCTGGGATTACAGGTACCCGCCACACACAGCTAAATTTGTATTTT	16320
Db	55708	CTCTCACTAGCTGGGATTACAGGTACCCGCCACACACAGCTAAATTTGTATTTT	55767
Qy	16321	AGTAGAGACAGGGTTTACCATGTTGGCCAGCGTCTCTCAAACTCTCACTTAAGTGA	16380
Db	55768	AGTAGAGACAGGGTTTACCATGTTGGCCAGCGTCTCTCAAACTCTCACTTAAGTGA	55827
Qy	16381	TCGCGCTCCCTCAGCCCTCCAAAGTGTGGGATTACAGGTGGAGCCACTACACACCC	16440
Db	55828	TCGCGCTCCCTCAGCCCTCCAAAGTGTGGGATTACAGGTGGAGCCACTACACACCC	55887
Qy	16441	AAGACTCTTTCAATTAACCAAGCATAGTCACTGCTTATGCCGTAAATCTAGCACTTA	16500
Db	55888	AAGACTCTTTCAATTAACCAAGCATAGTCACTGCTTATGCCGTAAATCTAGCACTTA	55947
Qy	16501	GGAGGCTGAGGTGGAGGATTTGGCTTACGCCAGGAGGTAAAGGCTGCAGTGTGCAG	16560
Db	55948	GGAGGCTGAGGTGGAGGATTTGGCTTACGCCAGGAGGTAAAGGCTGCAGTGTGCAG	56007
Qy	16561	CTGAATTTGCACTCTGCACATCCAGTCTGGAGACAGAAAGACCCGTCTCATTAATAA	16620
Db	56008	CTGAATTTGCACTCTGCACATCCAGTCTGGAGACAGAAAGACCCGTCTCATTAATAA	56067
Qy	16621	AAAAAATTAATTAATTTATCTTCAATTAACATCTTATTTGTGGCAGTCTATGT	16680
Db	56068	AAAAAATTAATTAATTTATCTTCAATTAACATCTTATTTGTGGCAGTCTATGT	56127
Qy	16681	CAGTGAATTAATCTGGGTGTAAAAATATCTCAAGAGTCTGTATTAAGTAATGGCTGAC	16740
Db	56128	CAGTGAATTAATCTGGGTGTAAAAATATCTCAAGAGTCTGTATTAAGTAATGGCTGAC	56187
Qy	16741	TTTGGAGATGAGAGATAGAAAAAGACACCTGTCTCATTTAAACAAAAAAGAAAAACAAA	16800
Db	56188	TTTGGAGATGAGAGATAGAAAAAGACACCTGTCTCATTTAAACAAAAAAGAAAAACAAA	56247
Qy	16801	ACACACCAAAAAAGATCTGTTTCAATTAACAGCTTATTTGTGGCAAGTCTATGTCAAG	16860

OY	10261	GATTTCACAAACCTGTGGCAGACAGTATGAAAGTACATGAGAAAGCTTTGTATCAGGA	10320
Db	49708	GATTTCACAAACCTGTGGCAGACAGTATGAAAGTACATGAGAAAGCTTTGTATCAGGA	49767
OY	10321	AAATCTTGAGGCGCAAGTAAACCTGCTTAGAGCTGAGTCTTCACTGCGAAACTCTAC	10380
Db	49768	AAATCTTGAGGCGCAAGTAAACCTGCTTAGAGCTGAGTCTTCACTGCGAAACTCTAC	49827
OY	10381	AGACTTTACACATGACAGAAAGTGTCCAAAAAGCATACATGATTAAGAAAGAACTCC	10440
Db	49828	AGACTTTACACATGACAGAAAGTGTCCAAAAAGCATACATGATTAAGAAAGAACTCC	49887
OY	10441	AGGAAAGGCAAAAGTAAATTCAAAAAGAAAGCTTGAGAAAGAGAGAGAAAAATGAAAA	10500
Db	49888	AGGAAAGGCAAAAGTAAATTCAAAAAGAAAGCTTGAGAAAGAGAGAGAAAAATGAAAA	49947
OY	10501	AATTAGACAGCTAAAGAAAGAAAGCAAAAAAGCGATACATTTTAAAGAAATATTCGC	10560
Db	49948	AATTAGACAGCTAAAGAAAGAAAGCAAAAAAGCGATACATTTTAAAGAAATATTCGC	50007
OY	10561	TATTCCTTGAGGTAAGTTAACTTTAGAAAGGTTGCTGTAGTACTTGAGGTTGTTCT	10620
Db	50008	TATTCCTTGAGGTAAGTTAACTTTAGAAAGGTTGCTGTAGTACTTGAGGTTGTTCT	50067
OY	10621	GCTCTGACATATTCCTTTGAAATGACTATTTTGTGTGAGAAATATTCCTCAATAGTAT	10680
Db	50068	GCTCTGACATATTCCTTTGAAATGACTATTTTGTGTGAGAAATATTCCTCAATAGTAT	50127
OY	10681	GTGATTTAAACTAACTGGTCTTGGCCAGGTGCATGCTGATGCTTAATCCAGAGAC	10740
Db	50128	GTGATTTAAACTAACTGGTCTTGGCCAGGTGCATGCTGATGCTTAATCCAGAGAC	50187
OY	10741	TTTGGAGGCTGAGGCCAGAGGCTACTTAAGCCAGAGATTGAGAAACAGCTAGGCA	10800
Db	50188	TTTGGAGGCTGAGGCCAGAGGCTACTTAAGCCAGAGATTGAGAAACAGCTAGGCA	50247
OY	10801	CAGACTGAGATCCCATCTCTACAAAAAATTTAAATATAGTTGGGTGTGGGCTCTACT	10860
Db	50248	CAGACTGAGATCCCATCTCTACAAAAAATTTAAATATAGTTGGGTGTGGGCTCTACT	50307
OY	10861	CCGAGCTGATCCCACTACTTGGAGGGTGGAGGTGAGAAATCATTGAGCCAGGAA	10920
Db	50308	CCGAGCTGATCCCACTACTTGGAGGGTGGAGGTGAGAAATCATTGAGCCAGGAA	50367
OY	10921	GTGAGGCTGCAATGAAAGCTTAATTTGACCACTGATCCAGCTGGATGACAGAGTGA	10980
Db	50368	GTGAGGCTGCAATGAAAGCTTAATTTGACCACTGATCCAGCTGGATGACAGAGTGA	50427
OY	10981	GACCTGTCTCAAAAAAACAACAAAAACAAAAACAAAAAATTTGCTTATAT	11040
Db	50428	GACCTGTCTCAAAAAAACAACAAAAACAAAAACAAAAAATTTGCTTATAT	50487
OY	11041	CTATTTGGGATGAGAGGACATTTCCAAATTAATGAGTTTCTGATTTCTTATAGCC	11100
Db	50488	CTATTTGGGATGAGAGGACATTTCCAAATTAATGAGTTTCTGATTTCTTATAGCC	50547
OY	11101	ACATGAGTAATTTCTTGTCTCTGAGCTGATGAAATTAATCTGAAAGAGCTTTT	11160
Db	50548	ACATGAGTAATTTCTTGTCTCTGAGCTGATGAAATTAATCTGAAAGAGCTTTT	50607
OY	11161	TATGATCTATGACATGATGATGTTGTTGCTTAACCTGAAAAACCAATCTCAATTTATA	11220
Db	50608	TATGATCTATGACATGATGATGTTGTTGCTTAACCTGAAAAACCAATCTCAATTTATA	50667
OY	11221	AACATGATGCTTAACAGTATTTTACTTCAAAAAAATTTAGCTTATTAAGTTAGT	11280
Db	50668	AACATGATGCTTAACAGTATTTTACTTCAAAAAAATTTAGCTTATTAAGTTAGT	50727
OY	11281	TTAGACAGTTGCAATTAACAACTTGACCTCAAAAGATATGATGATGATGAAACCA	11340
Db	50728	TTAGACAGTTGCAATTAACAACTTGACCTCAAAAGATATGATGATGATGAAACCA	50787
OY	11341	GTAAGATGTTCTAGATTTTATATGCTTGTCTGTGATGAACATGGGCTTTTCTGGCC	11400
Db	50788	GTAAGATGTTCTAGATTTTATATGCTTGTCTGTGATGAACATGGGCTTTTCTGGCC	50847
OY	11401	TCATCAAAATGGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11460
Db	50848	TCATCAAAATGGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	50907
OY	11461	TTTTCTTTATGATTTACTTAGAGAGATGATGATGATGATGATGATGATGATGATGAT	11520
Db	50908	TTTTCTTTATGATTTACTTAGAGAGATGATGATGATGATGATGATGATGATGATGAT	50967
OY	11521	CTCTTGAGGATTAAGAGGCTTTTGAACCTGTTGAGAGATGAAATTAACCTGCAATG	11580
Db	50968	CTCTTGAGGATTAAGAGGCTTTTGAACCTGTTGAGAGATGAAATTAACCTGCAATG	51027
OY	11581	GAGATGAGAGATGATTAAGATCAATTAAGAGAGATGATTAAGAGAGATGATTAAG	11640
Db	51028	GAGATGAGAGATGATTAAGATCAATTAAGAGAGATGATTAAGAGAGATGATTAAG	51087
OY	11641	AAGCAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11700
Db	51088	AAGCAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	51147
OY	11701	TTTTAATTTACTGTTGGAACCTTAATTTTCTTTTAACTGAGAGAAAGCTGTGCTGAT	11760
Db	51148	TTTTAATTTACTGTTGGAACCTTAATTTTCTTTTAACTGAGAGAAAGCTGTGCTGAT	51207
OY	11761	GACTTAAGCTGTTGAGCTGTTAATTTTGAAGACTTGACAGTACAGATGATGATGAT	11820
Db	51208	GACTTAAGCTGTTGAGCTGTTAATTTTGAAGACTTGACAGTACAGATGATGATGAT	51267
OY	11821	CTTCTTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11880
Db	51268	CTTCTTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	51327
OY	11881	TACATATTTGATGCTGTAGTAAGATCAGATTAATTAAGGAGAGATGATTAATTTG	11940
Db	51328	TACATATTTGATGCTGTAGTAAGATCAGATTAATTAAGGAGAGATGATTAATTTG	51387
OY	11941	CAATCCTATGAGCTTTGAGAAATGAACCTTATAGGCTTTGAGAGAGATGATTAAT	12000
Db	51388	CAATCCTATGAGCTTTGAGAAATGAACCTTATAGGCTTTGAGAGAGATGATTAAT	51447
OY	12001	GCATCAGTCAAAACATTTGTTGCCAGAGTGTGGAAGCATTAATTTTCTCTTAAGAT	12060
Db	51448	GCATCAGTCAAAACATTTGTTGCCAGAGTGTGGAAGCATTAATTTTCTCTTAAGAT	51507
OY	12061	TTTTTTAGCTTCTGCGAGTTATATCCCTTTTGAAGCAAGATGATTAACAGAGTAA	12120
Db	51508	TTTTTTAGCTTCTGCGAGTTATATCCCTTTTGAAGCAAGATGATTAACAGAGTAA	51567
OY	12121	AGAAATTAAGGCTGAGAGCTCATCTGAGATGATGATGATGATGATGATGATGATGAT	12180
Db	51568	AGAAATTAAGGCTGAGAGCTCATCTGAGATGATGATGATGATGATGATGATGATGAT	51627
OY	12181	GTTCTTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	12240
Db	51628	GTTCTTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	51687
OY	12241	GACTACAAAAAGTGTGCTGACGTAAGCAATCCCTTATTTGAATTTGTTTGTCTTAA	12300
Db	51688	GACTACAAAAAGTGTGCTGACGTAAGCAATCCCTTATTTGAATTTGTTTGTCTTAA	51747
OY	12301	TCACCTGCAATTTCTTTAGAAAAAAGAACATCTTGTGAGAGTGGGCTCCATTCATT	12360
Db	51748	TCACCTGCAATTTCTTTAGAAAAAAGAACATCTTGTGAGAGTGGGCTCCATTCATT	51807
OY	12361	GAGGAGGAGAGTGTATTAACAAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAG	12420
Db	51808	GAGGAGGAGAGTGTATTAACAAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAG	51867
OY	12421	TAGTCACTGATCTCTTTACACAGAGATTAATGATTTCTTAGAGATTAATTTTATAT	12480
Db	51868	TAGTCACTGATCTCTTTACACAGAGATTAATGATTTCTTAGAGATTAATTTTATAT	51927

47488	AAAAAGGAAATATACATATATAGCGGGCGTGGCTCAGCTCTGTAATCCACCACTTTG	47547
8101	GGAGGCTGAGCGGGCGGATCAGCTCAGCTCAGGAGTTGGAGACAGGCTGACTAACATG	8160
47548	GGAGGCTGAGCGGGCGGATCAGCTCAGCTCAGGAGTTGGAGACAGGCTGACTAACATG	47607
8161	GAGNAACCCCATCTCTACTAAAAATACAAAATAGCCAGACGTGCTGACACATGCTGTA	8220
47608	GAGNAACCCCATCTCTACTAAAAATACAAAATAGCCAGACGTGCTGACATGCTGTA	47667
8221	ATCCCAGCTACTCGGAGGCTGAGCGAGGAGAAATGCTTGAACCTGGGAGCGAGGTTG	8280
47668	ATCCCAGCTACTCGGAGGCTGAGCGAGGAGAAATGCTTGAACCTGGGAGCGAGGTTG	47727
8281	CGGTGAGCCGAGATCGGCGCTTGCCTCCATCTGGGCGACAACGGCAAAACCTCCATCT	8340
47728	CGGTGAGCCGAGATCGGCGCTTGCCTCCATCTGGGCGACAACGGCAAAACCTCCATCT	47787
8341	CAAAAAAGAAATATACACATAGCATATAGAAATATACATACATATATAATATATAG	8400
47788	CAAAAAAGAAATATACACATAGCATATAGAAATATACATACATATATAATATATAG	47847
8401	AAATATACATACCTACACACATATACATTCACCTATGTGTTAACTTCTTTATAGGTT	8460
47848	AAATATACATACCTACACACATATACATTCACCTATGTGTTAACTTCTTTATAGGTT	47907
8461	TCTCTCCCTCTCTTTTTTTTTTCTTTGCAATATTTGTTAAAGAAACGGCGGGTCGAG	8520
47908	TCTCTCCCTCTCTTTTTTTTTTCTTTGCAATATTTGTTAAAGAAACGGCGGGTCGAG	47967
8521	TGCTCATACCTGTAAATCCAGCATTTTGGGAGCGAGGTGGCGGATCACCTTGAGGTC	8580
47968	TGCTCATACCTGTAAATCCAGCATTTTGGGAGCGAGGTGGCGGATCACCTTGAGGTC	48027
8581	AGGAGTTTGCACCGGCTGGCCAGCATGGTGAACCTTGTCTCTATTAANTAGAAAA	8640
48028	AGGAGTTTGCACCGGCTGGCCAGCATGGTGAACCTTGTCTCTATTAANTAGAAAA	48087
8641	ATTAGCTGGGTGTGTGATGTGCGCTGTAAATCCAGCTACTCAGGAGGCTGAGGCAGGA	8700
48088	ATTAGCTGGGTGTGTGATGTGCGCTGTAAATCCAGCTACTCAGGAGGCTGAGGCAGGA	48147
8701	GAATCCGTTGAACCCAGGAGCGAGGTTGCAGTGAGCCGAGATTGCACCACTGCATCC	8760
48148	GAATCCGTTGAACCCAGGAGCGAGGTTGCAGTGAGCCGAGATTGCACCACTGCATCC	48207
8761	AGCCTGGGTGCAGAGCGAGATTCTCTCAAAAAAAGAGAGAGAGAGAGAGAGAGAG	8820
48208	AGCCTGGGTGCAGAGCGAGATTCTCTCAAAAAAAGAGAGAGAGAGAGAGAGAGAG	48267
8821	GAAGAACCACCCAGTTTGACTTGTAGAAATTTCCACGCTCAGATTGCATATCTGTGT	8880
48268	GAAGAACCACCCAGTTTGACTTGTAGAAATTTCCACGCTCAGATTGCATATCTGTGT	48327
8881	ATTATTACATGTTCCCTATTCCTCTATTCCCTATACTTGCCTAGTTAGATCTAGAG	8940
48328	ATTATTACATGTTCCCTATTCCTCTATTCCCTATACTTGCCTAGTTAGATCTAGAG	48387
8941	ACTTGATAGGATTCAAAATTTGATTTCTGTCGTCAGGAATCTTTATGCTAGTATGGGTA	9000
48388	ACTTGATAGGATTCAAAATTTGATTTCTGTCGTCAGGAATCTTTATGCTAGTATGGGTA	48447
9001	CTTCTATTAGGAGCACATAATGTCTGTTTCTCTTTTGGTGATGTTAGCAGCATTT	9060
48448	CTTCTATTAGGAGCACATAATGTCTGTTTCTCTTTTGGTGATGTTAGCAGCATTT	48507
9061	AATGATAATTGCTAGGTCGTTATTTAATTGAGGGTTGATAAANTTGCTAATCTAAT	9120
48508	AATGATAATTGCTAGGTCGTTATTTAATTGAGGGTTGATAAANTTGCTAATCTAAT	48567
9121	TCTATCATTTATTAAATTCATAGATATTTCTCTAAATAGAAACTTCCCTCATCAATTG	9180
48568	TCTATCATTTATTAAATTCATAGATATTTCTCTAAATAGAAACTTCCCTCATCAATTG	48627

QY	9181	TATG	GATATATTGGG	AACAGTTCACACAG	AAAAGGCATATAAATG	CTTGATTCTTTTC	9240
DB	48628	TATG	GATATATTGGG	AACAGTTCACACAG	AAAAGGCATATAAATG	CTTGATTCTTTTC	48687
QY	9241	ATTT	TTTTTTTTACCG	TTACTAAA	AGAGTTGGTTCGTTAG	CATCCTTCA	9300
DB	48688	ATTT	TTTTTTTTACCG	TTACTAAA	AGAGTTGGTTCGTTAG	CATCCTTCA	48747
QY	9301	ATGA	ACTTTTGTGTT	GTGTC	CAGTAATCTTAAATG	TCATCCCTTCA	9360
DB	48748	ATGA	ACTTTTGTGTT	GTGTC	CAGTAATCTTAAATG	TCATCCCTTCA	48807
QY	9361	GTAT	TGGTGCTTTCC	TTAGTTAG	TCAGGTTGATGATCC	CACGATGTTGTG	9420
DB	48808	GTAT	TGGTGCTTTCC	TTAGTTAG	TCAGGTTGATGATCC	CACGATGTTGTG	48866
QY	9421	TACT	TGGAGCTTTCCG	TCACGCTGCTGG	TCATATAAAGTAT	TATTTGTCATTTCT	9480
DB	48868	TACT	TGGAGCTTTCCG	TCACGCTGCTGG	TCATATAAAGTAT	TATTTGTCATTTCT	48927
QY	9481	ACCT	AGAAATCAATG	ACCCAAAGCTCAT	TTTCAAGAGGAGCAG	ATAGTCTCTCAGATA	9540
DB	48928	ACCT	AGAAATCAATG	ACCCAAAGCTCAT	TTTCAAGAGGAGCAG	ATAGTCTCTCAGATA	48987
QY	9541	GTGC	ACAGGCGCAG	CTATGA	AAACAATTTGGAC	CCCTTGAGTGAAGGAGGTTG	9600
DB	48988	GTGC	ACAGGCGCAG	CTATGA	AAACAATTTGGAC	CCCTTGAGTGAAGGAGGTTG	49047
QY	9601	TTTAT	TTTTAGGAATAG	GTTCGGGAGCC	TCAGTTCTAAGT	AGATGGAATGATTTCA	9660
DB	49048	TTTAT	TTTTAGGAATAG	GTTCGGGAGCC	TCAGTTCTAAGT	AGATGGAATGATTTCA	49107
QY	9661	ATTC	CTCTGATTTAT	TACATATTAAT	ATGCCCCATCCTAT	TGTTGTTTTATTA	9720
DB	49108	ATTC	CTCTGATTTAT	TACATATTAAT	ATGCCCCATCCTAT	TGTTGTTTTATTA	49167
QY	9721	CAAA	NTAACAGTGGTGT	TACCTTTT	TGAAACATGATTTAT	TGTTGAATGCTCAATAGCT	9780
DB	49168	CAAA	NTAACAGTGGTGT	TACCTTTT	TGAAACATGATTTAT	TGTTGAATGCTCAATAGCT	49227
QY	9781	ACCA	TATGCTCGTGT	TAATGCA	TTCATCCTCTATATAA	AGGAATTTAACACCTG	9840
DB	49228	ACCA	TATGCTCGTGT	TAATGCA	TTCATCCTCTATATAA	AGGAATTTAACACCTG	49287
QY	9841	AGGT	TAGAACACTTTT	TACACAT	TGTAATATACG	TATTTCCCGAGTAAGAC	9900
DB	49288	AGGT	TAGAACACTTTT	TACACAT	TGTAATATACG	TATTTCCCGAGTAAGAC	49347
QY	9901	ATTT	TTTCCCGAGGAAAT	GTTTTTT	TCAAAATGATTTTTAG	ATTTGCTTTGCTACAA	9960
DB	49348	ATTT	TTTCCCGAGGAAAT	GTTTTTT	TCAAAATGATTTTTAG	ATTTGCTTTGCTACAA	49407
QY	9961	TTCT	TAAACAGTAG	TCAGTAA	TTTTCACAA	TGTTATATATCACTTC	10020
DB	49408	TTCT	TAAACAGTAG	TCAGTAA	TTTTCACAA	TGTTATATATCACTTC	49467
QY	10021	TTCA	GAGATAGTGGG	ACTAGGAGGAG	CATCAATGATGGTAT	ATAATTAAGAA	10080
DB	49468	TTCA	GAGATAGTGGG	ACTAGGAGGAG	CATCAATGATGGTAT	ATAATTAAGAA	49527
QY	10081	TCCT	CCAGATT	TCAGATGA	AGAGATATTTG	TAGTAAGAGGTTG	10140
DB	49528	TCCT	CCAGATT	TCAGATGA	AGAGATATTTG	TAGTAAGAGGTTG	49587
QY	10141	ACA	AGACATGATTC	GGAACAGAGG	ACACAAATGC	CTCCAGAGAA	10200
DB	49588	ACA	AGACATGATTC	GGAACAGAGG	ACACAAATGC	CTCCAGAGAA	49647
QY	10201	CAGT	GCCGAGGAGG	AAATTA	AGAGCAATTTAT	ATGCTGGG	10260
DB	49648	CAGT	GCCGAGGAGG	AAATTA	AGAGCAATTTAT	ATGCTGGG	49707

QY	5881	AATGTATATCATTTTGTATTACTGAATTTTTTGAGACCTCAGCCACCCCTGTATTACTGGCC	5940
Db	45328	AATGTATATCATTTTGTATTACTGAATTTTTTGAGACCTCAGCCACCCCTGTATTACTGGCC	4538
QY	5941	TGCCCTTGAGCGTGGCTGCAAAATTCGCTAAGAATATTCGCTATTCAAGACACCCATT	6000
Db	45388	TGCCCTTGAGCGTGGCTGCAAAATTCGCTAAGAATATTCGCTATTCAAGACACCCATT	45447
QY	6001	CCTTGACCTGTCTGTTACCTAAATTCGCTTCACACTCAGCAAGAGAAATTAATGT	6060
Db	45448	CCTTGACCTGTCTGTTACCTAAATTCGCTTCACACTCAGCAAGAGAAATTAATGT	45507
QY	6061	TACTGCTTTGGATTTGTGAGAGATCATAGTCATATTAATTTCTAGCAATCCCA	6120
Db	45508	TACTGCTTTGGATTTGTGAGAGATCATAGTCATATTAATTTCTAGCAATCCCA	45566
QY	6121	GCATTTGGGAGGTTAAGCGCCGACATTTGCTTGAGCTCAAGGTTTGAACCAAGCTGC	6180
Db	45568	GCATTTGGGAGGTTAAGCGCCGACATTTGCTTGAGCTCAAGGTTTGAACCAAGCTGC	45627
QY	6181	ATAGAAAAACATGCGAAACCCGCCCTACAAAAAATTTAGCGCGGCTGGCT	6240
Db	45628	ATAGAAAAACATGCGAAACCCGCCCTACAAAAAATTTAGCGCGGCTGGCT	45687
QY	6241	GTGTCTCCAGCTACTCGCTCCACAGTACTCGGGTGGCTGAGAGAAATCTTTGGGC	6300
Db	45688	GTGTCTCCAGCTACTCGCTCCACAGTACTCGGGTGGCTGAGAGAAATCTTTGGGC	45747
QY	6301	CTGGAGCTGAAGGCTCCAGTGAAGCAATGATCCCTGCACATCGCACTCAGCCTTAGCTGACA	6360
Db	45748	CTGGAGCTGAAGGCTCCAGTGAAGCAATGATCCCTGCACATCGCACTCAGCCTTAGCTGACA	45807
QY	6361	GAGTGAGACACTGTATCAAAAAAAAAAATTTGTACCTTCATTCAAATCAATTAAT	6420
Db	45808	GAGTGAGACACTGTATCAAAAAAAAAAATTTGTACCTTCATTCAAATCAATTAAT	45866
QY	6421	AATTTTTTTTTTTTGAGAGCGGAGTCTGCTCTGTGGCCAGACTGAGTGCAGTGGCAC	6480
Db	45868	AATTTTTTTTTTTTGAGAGCGGAGTCTGCTCTGTGGCCAGACTGAGTGCAGTGGCAC	45927
QY	6481	AATCTCGGCTCAGCTGCMAATTCGTGTCCCGTGGATTAAGGATATTCGTGCCACCCAC	6540
Db	45928	AATCTCGGCTCAGCTGCMAATTCGTGTCCCGTGGATTAAGGATATTCGTGCCACCCAC	45987
QY	6541	CTGAGCAGCTGGGACTACAGGACACAGCACACGCCACAGCTAAATTTGTATTATTACT	6600
Db	45988	CTGAGCAGCTGGGACTACAGGACACAGCACACGCCACAGCTAAATTTGTATTATTACT	46047
QY	6601	AGATAGCGGGTTTTACTGTATTGGCCAGGCTAGTCTCGAATCTCTGACCTTGATCTCAC	6660
Db	46048	AGATAGCGGGTTTTACTGTATTGGCCAGGCTAGTCTCGAATCTCTGACCTTGATCTCAC	46107
QY	6661	CCACCTCGGCTCCCAAGTGTGGGATTAACAGGCTGAGACCCAGCACTGCTTGACCAATT	6720
Db	46108	CCACCTCGGCTCCCAAGTGTGGGATTAACAGGCTGAGACCCAGCACTGCTTGACCAATT	46167
QY	6721	AATTAATTTTTTGAGAAACCACTAGCTGAGGCTTTGCTGCTGTATTAAGATGATTC	6780
Db	46168	AATTAATTTTTTGAGAAACCACTAGCTGAGGCTTTGCTGCTGTATTAAGATGATTC	46227
QY	6781	ATATTTCTCCCTTATTATTAATAGTGAATTCAGAGCCCTGAGAACACTAAGAGGTAGACT	6840
Db	46228	ATATTTCTCCCTTATTATTAATAGTGAATTCAGAGCCCTGAGAACACTAAGAGGTAGACT	46287
QY	6841	TGCGATCTAGGGTTAGCTTTAAGGTCACATACATGATCAAGTCACTTAACACACCCCTCT	6900
Db	46288	TGCGATCTAGGGTTAGCTTTAAGGTCACATACATGATCAAGTCACTTAACACACCCCTCT	46347
QY	6901	CCTTAGGTTTTTAATTTGCGACTTTTTAACTGTCTTAATTAGAAAATTTTCAACACCTATAC	6960
Db	46348	CCTTAGGTTTTTAATTTGCGACTTTTTAACTGTCTTAATTAGAAAATTTTCAACACCTATAC	46407
QY	6961	AACCGTAGAAAGATGATTAATTAAGAACCATCACTTACTTCMACTACAGTTTGAATATC	7020

[illegible]

Db	43108	TAAAGGTAGATGCCCTCTAGGAGTGATGAGTGGTTTCTACATCCTCAAAATTAACCTCTAC	43167	QY	4801	GGACCTCCACTCTGGCTGGCGGAAAGCAAGACAGCACTGCTGGCTGGAGACGGCGG	4860
QY	3721	AGAGAAATTAAGATTATCCAAACCATATTTTGGTATCTGAGCAGCCGCCACAAAATTTT	3780	Db	44248	GGACCTCCACTCTGGCTGGCGGAAAGCAAGACAGCACTGCTGGCTGGAGACGGCGG	44307
Db	43168	AGAGAAATTAAGATTATCCAAACCATATTTTGGTATCTGAGCAGCCGCCACAAAATTTT	43227	QY	4861	GACCGCTGCTCTCCGGCTGAGGAAATCAGAGACAGCTCCGCTCCCTAGTGGAGCGGAGG	4920
QY	3781	TTTCTTTAGAGACAGGTCTCCCTCTATCGCTACGCTGAAGTGCAGTGGTGGATCATA	3840	Db	44308	GAGCGCTGCTCTCCGGCTGAGGAAATCAGAGACAGCTCCGCTCCCTAGTGGAGCGGAGG	44367
Db	43228	TTTCTTTAGAGACAGGTCTCCCTCTATCGCTACGCTGAAGTGCAGTGGTGGATCATA	43287	QY	4921	GAGCGAAGTCTATGACAGCGGAGTGGGTCTGAGGTGAGTTTATGCACACGCCGCCCA	4980
QY	3841	ACTCACTCTAACCTCAAACTCCCTGGACTAAGCCATCTCCACCTCGGCTCCCAAGC	3900	Db	44368	GAGCGAAGTCTATGACAGCGGAGTGGGTCTGAGGTGAGTTTATGCACACGCCGCCCA	44427
Db	43288	ACTCACTCTAACCTCAAACTCCCTGGACTAAGCCATCTCCACCTCGGCTCCCAAGC	43347	QY	4981	CGGGGCTTTAGAAAGCGCGGACCGAGAGTTAGTGGGGCGGGGTAGACCCCGCTGAC	5040
QY	3901	GTTCAGATTACAAGCGTAGCCATGAGAGCCGCGCTCTTTAAAAATAAAGTGGGCGG	3960	Db	44428	CGGGGCTTTAGAAAGCGCGGACCGAGAGTTAGTGGGGCGGGGTAGACCCCGCTGAC	44487
Db	43348	GTTCAGATTACAAGCGTAGCCATGAGAGCCGCGCTCTTTAAAAATAAAGTGGGCGG	43407	QY	5041	CCGAGCGCGCGGGCGGAGGACTGCGGTCTCCGGGCTTCGGCGCGCGGCTCCCGCGG	5100
QY	3961	GGCACAGTGGCTCACGCTGTGAGGGTATGAGGCTTCCAGCAGCTTTGGAGGCGCGAGG	4020	Db	44488	CCGAGCGCGCGGGCGGAGGACTGCGGTCTCCGGGCTTCGGCGCGCGGCTCCCGCGG	44547
Db	43408	GGCACAGTGGCTCACGCTGTGAGGGTATGAGGCTTCCAGCAGCTTTGGAGGCGCGAGG	43467	QY	5101	CTCCAGACTCGGCGCGGATGGGTTCGACCGGGCATCCCGTCCCGCGCGCGGCTTCGCG	5160
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2161 AAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
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		Db	40888	AGAAAAAGAAAGAAATTTCTGAAGATTTGTTGATTTGATTAACAAATTTGAATGTACTT	40947

AUTHORS
TITLE

Howden, P.
Direct Submission
Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humphrys@sanger.ac.uk; Clone
requests: clonerequest@sanger.ac.uk

COMMENT

On Sep 19, 2000 this sequence version replaced g1:9714820.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone configs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
This sequence is the entire insert of clone RP11-43507. The true
left end of clone RP1-6283 is at 123829 in this sequence. The true
right end of clone RP4-55523 is at 81044 in this sequence. This
sequence has been finished according to sequence map criteria as
follows: An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
RP11-43507 is from the library RPI1-11.2 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6.

FEATURES

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gene

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 14:54:01 ; Search time 48642 Seconds
(without alignments)
17949.183 Million cell updates/sec

Title: US-09-982-091A-5_COPY_1_30000
Perfect score: 30000
Sequence: 1 aagcaggtagtttaactt.....taataaaaaataagaatgacc 30000

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:

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2: gb.htg:*
3: gb.in:*
4: gb.in:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
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11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
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21: em.or:*
22: em.ov:*
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25: em.pl:*
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27: em.sts:*
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31: em.htg_inv:*
32: em.htg_other:*
33: em.htg_mus:*
34: em.htg_pln:*
35: em.htg_rod:*
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37: em.htg_vrt:*
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41: em.htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	10530	35.1	111862	2	AL139143	AL139143 Homo sapi
3	575	1.9	4756	9	AF297866	AF297866 Homo sapi
c	487	1.6	193690	2	AC118559	AC118559 Homo sapi
5	231	0.8	421	6	AX246208	AX246208 Sequence
6	197	0.7	422	6	AX246209	AX246209 Sequence
7	173	0.6	393	6	AX245923	AX245923 Sequence
8	164	0.5	408	6	AX245847	AX245847 Sequence
9	138	0.5	411	6	AX071922	AX071922 Sequence
10	135	0.4	386	6	AX069706	AX069706 Sequence
11	133	0.4	406	6	AX071923	AX071923 Sequence
12	113	0.4	174562	2	AC005848	AC005848 Homo sapi
13	112	0.4	221475	9	AC009562	AC009562 Homo sapi
14	109	0.4	127661	2	AP001261	AP001261 Homo sapi
15	109	0.4	160535	9	AP000729	AP000729 Homo sapi
c	109	0.4	199522	9	AC089999	AC089999 Homo sapi
17	106	0.4	164684	9	AL590683	AL590683 Human DNA
c	105	0.4	38897	9	AC021092	AC021092 Homo sapi
19	105	0.4	156321	9	AC074331	AC074331 Homo sapi
c	104	0.3	43507	9	AF305057	AF305057 Homo sapi
21	104	0.3	152711	9	AP001178	AP001178 Homo sapi
c	103	0.3	147250	2	AC011778	AC011778 Homo sapi
23	103	0.3	177743	9	AC105941	AC105941 Homo sapi
24	103	0.3	189441	2	AC022989	AC022989 Homo sapi
25	102	0.3	89251	9	HSJ3812P3	AL121909 Human DNA
26	101	0.3	139118	9	AL133477	AL133477 Human DNA
27	101	0.3	165584	9	AC015922	AC015922 Homo sapi
c	101	0.3	185415	9	HS121M24	AL354046 Homo sapi
29	99	0.3	164306	2	AP002785	AP002785 Homo sapi
c	99	0.3	170172	2	AC104765	AC104765 Homo sapi
31	99	0.3	187190	2	AC026898	AC026898 Homo sapi
c	98	0.3	308676	2	AC068639	AC068639 Homo sapi
33	97	0.3	131753	9	AL358790	AL358790 Human DNA
34	97	0.3	151445	9	AL354943	AL354943 Human DNA
c	97	0.3	160460	2	AC024374	AC024374 Homo sapi
36	97	0.3	161536	2	AC024318	AC024318 Homo sapi
37	97	0.3	167981	2	AL591856	AL591856 Homo sapi
c	97	0.3	169089	9	AC008537	AC008537 Homo sapi
39	97	0.3	173758	9	AC009144	AC009144 Homo sapi
c	97	0.3	192016	2	AC026540	AC026540 Homo sapi
41	97	0.3	216215	9	HSG256022	AL080239 Human DNA
c	97	0.3	237613	2	AC025769	AC025769 Homo sapi
43	96	0.3	72045	9	AC092214	AC092214 Homo sapi
44	96	0.3	103056	9	AC068447	AC068447 Homo sapi
c	95	0.3	104794	9	AC104046	AC104046 Homo sapi

ALIGNMENTS

RESULT 1
AL354864
LOCUS
DEFINITION
Human DNA sequence from clone RP11-435D7 on chromosome 1. Contains ESTs, STSS, GSSs and Cpg islands. Contains a novel gene and the 5' part of the PSMB2 gene for proteasome (prosome, macropain) subunit 2, beta type, complete sequence.
ACCESSION
AL354864
VERSION
AL354864.16 GI:10185566
KEYWORDS
HTG; Cpg island; macropain; prosome; proteasome; PSMB2.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 194296)

Db 415 GTGGTCTGGCAGCTCTGCTCCCTCTCGAGACAACGGCTATGCCAGCTTCCTCTGA 474
 QY 28837 G 28837
 Db 475 G 475

AX333105 466 bp DNA Linear PAT 09-JAN-2002
 Sequence 3614 from Patent WO0194629.
 AX333105
 VERSION AX333105.1 GI:18123739
 LOCUS
 DEFINITION
 ACCESSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 TITLE
 Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL
 Patent: WO 0194629-A 3614 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 FEATURES
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 BASE COUNT 143 a 90 c 103 g 129 t 1 others
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QY 9489 GAATTAATTTTCTGCTCTTAATAAGGACTTAACTGGTACCCCAAGTCAGAAAGACTCTGC 9548
 Db 340 GAATTAATTTTCTGCTCTTAATAAGGACTTAACTGGTACCCCAAGTCAGAAAGACTCTGC 281
 QY 9549 CTCATAATTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 9608
 Db 280 CTCATAATTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 221
 QY 9609 CAGCTGTGGGGCAGAGACCCCTTCTGGGACTGAATTCATATTTGAAGCACTGTGT 9668
 Db 220 CAGCTGTGGGGCAGAGACCCCTTCTGGGACTGAATTCATATTTGAAGCACTGTGT 161
 QY 9669 TCAAGATCTCCCTCTGGGCTCTGACAGAAGAAACATAACCCCTTATTTGCAATCTT 9728
 Db 160 TCAAGATCTCCCTCTGGGCTCTGACAGAAGAAACATAACCCCTTATTTGCAATCTT 101
 QY 9729 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTGACATTTTCACTAATTT 9788
 Db 100 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTGACATTTTCACTAATTT 41
 QY 9789 TGAGAAGGCCACCATGGAATTTAATAAAATATTATTG 9828
 Db 40 TGAGAAGGCCACCATGGAATTTAATAAAATATTATTG 1

RESULT 7
 G30470/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human STS SHGC-37119, sequence tagged site.
 G30470
 G30470.1 GI:1594021
 STS; STS sequence; primer; sequence tagged site.
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 466)

AUTHORS JOURNAL COMMENT

Myers, R.M.
 Unpublished (1996)

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu

Primer A: TTATTAATTTCCATGGTGGCC
 Primer B: CCTTCTGGGTCTGACAAGA
 STS size: 140
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from N72576
 -- Washington University/Merck EST sequence.

FEATURES
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 /db_xref="taxon:9606"
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 11..150
 primer_bind
 complement(131..150)
 BASE COUNT 143 a 90 c 103 g 129 t 1 others
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 Best Local Similarity 100.0%; Pred. No. 1e-164;
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 Db 340 GAATTAATTTTCTGCTCTTAATAAGGACTTAACTGGTACCCCAAGTCAGAAAGACTCTGC 281
 QY 9549 CTCATAATTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 9608
 Db 280 CTCATAATTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 221
 QY 9609 CAGCTGTGGGGCAGAGACCCCTTCTGGGACTGAATTCATATTTGAAGCACTGTGT 9668
 Db 220 CAGCTGTGGGGCAGAGACCCCTTCTGGGACTGAATTCATATTTGAAGCACTGTGT 161
 QY 9669 TCAAGATCTCCCTCTGGGCTCTGACAGAAGAAACATAACCCCTTATTTGCAATCTT 9728
 Db 160 TCAAGATCTCCCTCTGGGCTCTGACAGAAGAAACATAACCCCTTATTTGCAATCTT 101
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 Db 100 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTGACATTTTCACTAATTT 41
 QY 9789 TGAGAAGGCCACCATGGAATTTAATAAAATATTATTG 9828

Db		40	TGACAGAACGCCCAATGCATTATAAATAATATATATC 1
RESULT #			
LOCUS			
AK096466		2394 bp	mRNA linear PRI 15-JUL-2002
DEFINITION			Homo sapiens cDNA FLJ39147 fis, clone OCBBF2000523.
ACCESSION			AK096466
VERSION			AK096466.1 GI:21755971
KEYWORDS			cDNA capping; fis (full insert sequence).
SOURCE			Homo sapiens fetal brain cDNA to mRNA, clone_1lib:OCBBF2 clone:OCBBF2000523.
ORGANISM			Homo sapiens
REFERENCE			Eukaryote: Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS			1
			Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Matanabe, S., Ishida, S., Ono, I., Holuta, T., Matanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Salto, K., Mishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takashima-Fujii, A., Oshima, A., Sugiyama, Y., Kawakami, B., Suzuki, Y., Sugano, S., Negahari, K., Masuh, Y., Nagai, K. and Isogai, T.
JOURNAL			NEDO human cDNA sequencing project
REFERENCE			Unpublished
AUTHORS			2 (bases 1 to 2394)
TITLE			Isogai, T. and Yamamoto, J.
JOURNAL			Direct Submission
			Submitted (04-JUL-2002) Takao Isogai, Flj Project(HRI Team); 2-6-7 Kazuo-Kamachi, Kisarazu, Chiba 292-0812, Japan (e-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biochemistry (RAB) (cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-63'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. Location/Qualifiers
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			/protein_id="BAC04799.1"
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CDS			
			BASE COUNT 560 a 340 c 705 g 589 t
ORIGIN			
			Query Match 1.0%; Score 299; DB 9; Length 2394;
			Best Local Similarity 100.0%; Pred. No. 18e-143;
			Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy			28539 CCTGCATTATGTCCAGCCCCGAGCTTCACAACAGACAGCAACTTCATGGCAAGTCCC 28559
Dd			8 CCTGGATTATGTCCAGCCCCGAGCTTCACAACAGACAGCAACTTCATGGCAAGTCCC 67
Oy			28559 AAGATGCTTAACGAAGAAATGGCATGGGATGTCAGCACGAGTGGAAGCACTATCTCAGAGG 28655
Dd			68 AAGATGCTTAACGAAGAAATGGCATGGGATGTCAGCACGAGTGGAAGCACTATCTCAGAGG 127

[illegible]

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/db_xref="taxon:9606"
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/clone="CTD-2052B23"
/clone_lib="CITD1 Human"
1. .6251
/note="assembly fragment"
ture
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Summary Statistics		
Sequencing vector:	M13; M77815;	100% of reads
Chemistry:	Dye-terminator Big Dye;	100% of reads
Assembly program:	Phrap;	version 0.960731
Consensus quality:	140178 bases at	least 0.40
Consensus quality:	150137 bases at	least 0.30
Consensus quality:	154209 bases at	least 0.20
Insert size:	188000;	agarose-1p
Insert size:	157413;	sum-of-contigs
Quality coverage:	3.0 in Q20 bases;	agarose-1p
Quality coverage:	3.5 in Q20 bases;	sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	1309:	contig of 1309 bp	in length
1310	1409:	gap of 100 bp	
1410	2462:	contig of 1053 bp	in length
2463	2562:	gap of 100 bp	
2563	3707:	contig of 1145 bp	in length
3708	3807:	gap of 100 bp	
3808	4998:	contig of 1191 bp	in length
4999	5098:	gap of 100 bp	
5099	6927:	contig of 1829 bp	in length
6928	7027:	gap of 100 bp	
7028	8933:	contig of 1906 bp	in length
8934	9033:	gap of 100 bp	
9034	10733:	contig of 1700 bp	in length
10734	10833:	gap of 100 bp	
10834	12128:	contig of 1295 bp	in length
12129	12228:	gap of 100 bp	
12229	14227:	contig of 1999 bp	in length
14228	14327:	gap of 100 bp	
14328	16144:	contig of 1817 bp	in length
16145	16244:	gap of 100 bp	
16245	17544:	contig of 1300 bp	in length
17545	17644:	gap of 100 bp	
17645	19728:	contig of 2084 bp	in length
19729	19828:	gap of 100 bp	
19829	21896:	contig of 2068 bp	in length
21897	21996:	gap of 100 bp	
21997	22660:	contig of 1664 bp	in length
23661	23760:	gap of 100 bp	
23761	27013:	contig of 3253 bp	in length
27014	27113:	gap of 100 bp	
27114	29667:	contig of 2554 bp	in length
29668	29767:	gap of 100 bp	
29768	33523:	contig of 2756 bp	in length
33524	32623:	gap of 100 bp	
32624	36050:	contig of 3427 bp	in length
36051	36150:	gap of 100 bp	
36151	37488:	contig of 1338 bp	in length
37489	37588:	gap of 100 bp	
37589	40082:	contig of 2494 bp	in length
40083	40182:	gap of 100 bp	
40183	42408:	contig of 3226 bp	in length
43409	43508:	gap of 100 bp	
43509	46386:	contig of 2878 bp	in length
46387	46486:	gap of 100 bp	
46487	50157:	contig of 3671 bp	in length
50158	50257:	gap of 100 bp	
50258	53228:	contig of 2971 bp	in length
53229	53328:	gap of 100 bp	
53329	56167:	contig of 2839 bp	in length
56168	56267:	gap of 100 bp	
56268	61644:	contig of 5377 bp	in length
61645	61744:	gap of 100 bp	
61745	65196:	contig of 3452 bp	in length

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* 65197 65296: gap of 100 bp
* 65297 70157: contig of 4861 bp in length
* 70158 70257: gap of 100 bp
* 70258 74554: contig of 4297 bp in length
* 74555 74654: gap of 100 bp
* 74655 79228: contig of 4574 bp in length
* 79229 79328: gap of 100 bp
* 79329 84640: contig of 5312 bp in length
* 84641 84740: gap of 100 bp
* 84741 89974: contig of 5234 bp in length
* 89975 90074: gap of 100 bp
* 90075 96883: contig of 6809 bp in length
* 96884 96983: gap of 100 bp
* 96984 102058: contig of 5075 bp in length
* 102059 102158: gap of 100 bp
* 102159 107640: contig of 5482 bp in length
* 107641 107740: gap of 100 bp
* 107741 113941: contig of 6201 bp in length
* 113942 114041: gap of 100 bp
* 114042 118500: contig of 4459 bp in length
* 118501 118600: gap of 100 bp
* 118601 125732: contig of 7132 bp in length
* 125733 125832: gap of 100 bp
* 125833 132596: contig of 6764 bp in length
* 132597 132696: gap of 100 bp
* 132697 139895: contig of 7199 bp in length
* 139896 147426: contig of 7431 bp in length
* 147427 147526: gap of 100 bp
* 147527 153241: contig of 5715 bp in length
* 153242 153341: gap of 100 bp
* 153342 161613: contig of 8272 bp in length.

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FEATURES

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2563..3707
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3808..4998
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5099..6927
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9034..10733
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 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24149 CCACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGC 24193
 |||||
 Db 107016 CCACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGC 106972

RESULT 12
 AC092450.4

WPCOMMENT

Sequence split into 8 fragments LOCUS AC092450 Accession AC092450

Fragment Name	Begin	End
AC092450_0	1	110000
AC092450_1	100001	210000
AC092450_2	200001	310000
AC092450_3	300001	410000
AC092450_4	400001	510000
AC092450_5	500001	610000
AC092450_6	600001	710000
AC092450_7	700001	727300

Continuation (5 of 8) of AC092450 from base 400001 (AC092450 Homo sapiens chromosome

Query Match 0.9%; Score 246; DB 2; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 5e-116;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24149 CCACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGCTG 24195
 |||||
 Db 39351 CCACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGCTG 39397

RESULT 13
 AC092450.6/c

WPCOMMENT

Sequence split into 8 fragments LOCUS AC092450 Accession AC092450

Fragment Name	Begin	End
AC092450_0	1	110000
AC092450_1	100001	210000
AC092450_2	200001	310000
AC092450_3	300001	410000
AC092450_4	400001	510000
AC092450_5	500001	610000
AC092450_6	600001	710000
AC092450_7	700001	727300

Continuation (7 of 8) of AC092450 from base 600001 (AC092450 Homo sapiens chromosome

Query Match 0.9%; Score 246; DB 2; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 5e-116;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25090 TCTTGGCTCACTGCAACCTCCACCTCCAGGTTCAAGCGATTCTCTGCTCAGGCTCCC 25149
 |||||
 Db 88212 TCTTGGCTCACTGCAACCTCCACCTCCAGGTTCAAGCGATTCTCTGCTCAGGCTCCC 88153

RESULT 14
 HSJ231p7P/c

LOCUS

DEFINITION Human DNA sequence from clone 231p7p on chromosome 22q11.21-12.2

Contains CA repeat and STS, complete sequence.

ACCESSION AL096757

VERSION 1.0

KEYWORDS HTG: repeat polymorphism.

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

HSJ231p7P 80485 bp DNA linear PRI 26-JUL-1999

REFERENCE 1 (bases 1 to 80485)
 AUTHORS Corby,N.
 TITLE Direct Submission
 JOURNAL Submitted (26-Jul-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 COMMENT During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>
 231P7P is from the library Rpci1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://pacpac.med.buffalo.edu/VECTOR:pcypac2> This sequence is the entire insert of clone 231P7P.
 FEATURES
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 2840..2890
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 2930..3016
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 repeat_region
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 5280..5343

/note="2 copies 32 mer 91% conserved"
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 5284..5343
 /note="15 copies 4 mer ca ca 97% conserved"
 repeat_region
 5284..5341
 /note="29 copies 2 mer ca 98% conserved"
 repeat_region
 5344..5637
 /note="AluSg repeat: matches 1..284 of consensus"
 repeat_region
 5687..5897
 /note="ORSL repeat: matches 243..459 of consensus"
 repeat_region
 5926..6013
 /note="MIR repeat: matches 46..136 of consensus"
 repeat_region
 6469..6733
 /note="AluY repeat: matches 42..304 of consensus"
 repeat_region
 7892..8202
 /note="AluY repeat: matches 1..311 of consensus"
 repeat_region
 8262..8454
 /note="MLT1G repeat: matches 283..512 of consensus"
 repeat_region
 8611..8719
 /note="MLT1G repeat: matches 9..112 of consensus"
 repeat_region
 8734..8854
 /note="L2 repeat: matches 2596..2740 of consensus"
 repeat_region
 9812..9891
 /note="MIR repeat: matches 36..119 of consensus"
 repeat_region
 10128..10489
 /note="L2 repeat: matches 1768..2187 of consensus"
 repeat_region
 10559..10644
 /note="43 copies 2 mer cc 63% conserved"
 repeat_region
 10755..10917
 /note="L2 repeat: matches 2543..2710 of consensus"
 repeat_region
 11250..11287
 /note="L1PA8 repeat: matches 5953..5990 of consensus"
 repeat_region
 11361..11663
 /note="AluX repeat: matches 1..295 of consensus"
 repeat_region
 11679..11786
 /note="MIR repeat: matches 21..147 of consensus"
 repeat_region
 12268..12395
 /note="MIR repeat: matches 118..262 of consensus"
 repeat_region
 12723..12774
 /note="MIR repeat: matches 210..261 of consensus"
 repeat_region
 12779..12818
 /note="10 copies 4 mer acac 93% conserved"
 repeat_region
 12779..12816
 /note="19 copies 2 mer ac 95% conserved"
 repeat_region
 13045..13151
 /note="MER91C repeat: matches 1..119 of consensus"
 repeat_region
 13227..13530
 /note="AluY repeat: matches 1..304 of consensus"
 repeat_region
 13997..14081
 /note="MIR repeat: matches 53..139 of consensus"
 repeat_region
 14935..14998
 /note="MIR repeat: matches 80..144 of consensus"
 repeat_region
 15852..15891
 /note="20 copies 2 mer gt 93% conserved"
 repeat_region
 15945..16336
 /note="L2 repeat: matches 2095..2490 of consensus"
 repeat_region
 16883..17092
 /note="MIR repeat: matches 39..252 of consensus"
 repeat_region
 17787..18087
 /note="AluX repeat: matches 2..303 of consensus"
 repeat_region
 18342..18505
 /note="MIR repeat: matches 103..262 of consensus"
 repeat_region
 18879..19024
 /note="MIR repeat: matches 47..197 of consensus"
 repeat_region
 19560..19815
 /note="2 copies 128 mer 80% conserved"
 repeat_region
 20108..20306
 /note="MIR repeat: matches 47..260 of consensus"
 repeat_region
 20430..20615
 /note="L2 repeat: matches 2308..2498 of consensus"
 repeat_region
 20902..20986
 /note="MIR repeat: matches 107..192 of consensus"
 repeat_region
 22071..22138
 /note="MIR repeat: matches 77..146 of consensus"

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repeat_region 22319..22418
/note="AluY repeat: matches 202..302 of consensus"
repeat_region 22474..22735
/note="L2 repeat: matches 2469..2750 of consensus"
repeat_region 22736..23023
/note="AluSp repeat: matches 1..289 of consensus"
repeat_region 23024..23042
/note="L2 repeat: matches 2453..2469 of consensus"
repeat_region 23412..23504
/note="MIR repeat: matches 46..143 of consensus"
repeat_region 23905..24045
/note="47 copies 3 mer atg 89% conserved"
repeat_region 23907..24290
/note="3 copies 128 mer 78% conserved"
repeat_region 24050..24151
/note="34 copies 3 mer gat 80% conserved"
repeat_region 24991..25077
/note="MIR repeat: matches 47..143 of consensus"
repeat_region 25282..25458
/note="L2 repeat: matches 2364..2418 of consensus"
repeat_region 25563..25957
/note="MSTO repeat: matches 1..394 of consensus"
repeat_region 26295..26604
/note="LIME1 repeat: matches 5505..5826 of consensus"
repeat_region 26705..26855
/note="L2 repeat: matches 2588..2749 of consensus"
repeat_region 26901..26972
/note="18 copies 4 mer gatg 72% conserved"
repeat_region 27383..27676
/note="AluX repeat: matches 1..296 of consensus"
repeat_region 27678..27854
/note="MIR repeat: matches 67..257 of consensus"
repeat_region 28123..28190
/note="MIR repeat: matches 109..183 of consensus"
repeat_region 28597..28750
/note="L2 repeat: matches 2591..2750 of consensus"
repeat_region 30377..30691
/note="AluDo repeat: matches 1..309 of consensus"
repeat_region 30692..31007
/note="MIR repeat: matches 49..366 of consensus"
repeat_region 31452..31588
/note="MIR repeat: matches 46..192 of consensus"
repeat_region 31843..31902
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 ACCESSION AC008999
 VERSION AC008999.7 GI:15281189

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 39707)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 39707)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint

REFERENCE 3 (bases 1 to 39707)
 AUTHORS Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 TITLE Direct Submission
 JOURNAL Submitted (03-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 4 (bases 1 to 39707)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (26-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 5 (bases 1 to 39707)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Aug 23, 2001 this sequence version replaced gi:11079409.
 Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: phrap Quality >=40 100% of Sequence;

Estimated Total Number of Errors is 0.

FEATURES

source

1..39707

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 Db 8469 GGAGCTGAGCGAGGAGGATCGCTTGAACCCGGAGGTGGAGTTGC 8515

Search completed: June 24, 2003, 22:16:23

Job time : 92791 secs